

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:42:00 ; Search time 1894 seconds
(without alignments)
13623.242 Million cell updates/sec

Title: US-09-598-443-1
Perfect score: 1233
Sequence: 1 atgcgaagtgctgtgatag.....tgtccaagatgatatgtag 1233

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Sealed: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb.ba:*
- 2: gb.htg:*
- 3: gb.in:*
- 4: gb.om:*
- 5: gb.ov:*
- 6: gb.pat:*
- 7: gb.ph:*
- 8: gb.pl:*
- 9: gb.pr:*
- 10: gb.ro:*
- 11: gb.sts:*
- 12: gb.sy:*
- 13: gb.un:*
- 14: gb.vl:*
- 15: em.ba:*
- 16: em.fun:*
- 17: em.hum:*
- 18: em.in:*
- 19: em.mu:*
- 20: em.om:*
- 21: em.or:*
- 22: em.ov:*
- 23: em.pat:*
- 24: em.ph:*
- 25: em.pl:*
- 26: em.ro:*
- 27: em.sts:*
- 28: em.un:*
- 29: em.vl:*
- 30: em.htg.hum:*
- 31: em.htg.inv:*
- 32: em.htg.other:*
- 33: em.htgc.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1233	100.0	1627	9	BC003591	BC003591 Homo sapi
2	1233	100.0	1695	9	AK025099	AK025099 Homo sapi
3	1231.4	99.9	1659	6	AX058610	AX058610 Sequence
4	1071.8	86.9	1649	6	AX201368	AX201368 Sequence
5	860.2	69.8	1568	10	BC010806	BC010806 Mus muscu
6	856.6	69.5	1421	10	AF239957	AF239957 Mus muscu
7	826	67.0	1540	10	AF113795	AF113795 Mus muscu
8	141.6	11.5	61326	2	AC108908	AC108908 Mus muscu
9	122	9.9	324	11	G38549	G38549 SHGC-64262
10	113	9.2	62831	2	AC109272	AC109272 Mus muscu
11	73.6	6.0	61326	2	AC108908	AC108908 Mus muscu
12	68	5.5	125020	2	AF429315	AF429315 Homo sapi
13	65.4	5.3	110000	2	AC091454_2	Continuation (3 of
14	64	5.2	145936	2	AC105364	AC105364 Oryza sat
15	63	5.1	207683	2	AC098712	AC098712 Mus muscu
16	62.6	5.1	125020	2	AF429315	AF429315 Homo sapi
17	60.2	4.9	318930	2	AC073495	AC073495 Mus muscu
18	59	4.8	241432	10	AL589661	AL589661 Mouse DNA
19	58.6	4.8	120598	2	OSJN00104	AL606653 Oryza sat
20	58.6	4.8	142799	2	OSJN00149	AL663017 Oryza sat
21	57	4.6	451	10	M581R3E2	M10668 Mouse DNA w
22	57	4.6	156654	8	AC074283	AC074283 Oryza sat
23	56.8	4.6	110000	2	LMFLCHR36_31	Continuation (32 o
24	56.8	4.6	175296	2	AC106674	AC106674 Rattus no
25	56.6	4.6	110000	2	LMFLCHR32_06	Continuation (7 of
26	56.4	4.6	1150	14	HS4ULIR3	J02079 epstein-bar
27	56.4	4.6	1818	9	G0RINVOLB	M23604 Gorfilla gor
28	56.4	4.6	1926	6	AX107940	AX107940 Sequence
29	56.4	4.6	2580	6	AR108994	AR108994 Sequence
30	56.4	4.6	5452	6	AR083151	AR083151 Sequence
31	56.4	4.6	5452	12	U02454	U02454 Cloning vec
32	56.4	4.6	9600	6	A92665	A92665 Sequence 1
33	56.4	4.6	9600	6	AR158345	AR158345 Sequence
34	56.4	4.6	10596	6	I25041	I25041 Sequence 15
35	56.4	4.6	10596	6	I30503	I30503 Sequence 15
36	56.4	4.6	10737	12	XXU02428	U02428 Cloning vec
37	56.4	4.6	10850	12	U02455	U02455 Cloning vec
38	56.4	4.6	172281	14	EBV	V01555 Epstein-Bar
39	56.4	4.6	184113	14	HS4B958RAJ	M80517 Epstein-Bar
40	55.8	4.5	38543	1	SCBAC16H6	AL596162 Streptomy
41	55.8	4.5	192675	14	AL589767	AL589767 Mouse DNA
42	55.6	4.5	229896	10	AF232689	AF232689 Rat cytom
43	55.2	4.5	1458	8	AF387790	AF387790 Sorghum b
44	55.2	4.5	138070	2	AC109783	AC109783 Mus muscu
45	55.2	4.5	224061	2	AL606909	AL606909 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS BC003591
DEFINITION Homo sapiens, single Ig IL-1R-related molecule, clone MGC:4338
IMAGE:2821373, mRNA, complete cds.
ACCESSION BC003591
VERSION BC003591.1 GI:13097794
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 1627)
AUTHORS Strausberg/R.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP

AUTHORS Kawabata,A., Hiki,J.I., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE MEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 1695)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-Ku, TOKYO 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT MEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES
source location/Qualifiers

1..1695
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COL4458"
/tissue_type="colon"
/clone_lib="COL"
/note="cloning vector pME18SFL3"
227..1459
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB15066.1"
/db_xref="GI:10437547"
/translation="MPGYCDRAPDPLSPEDVYLRPALSSVAIACIAWVSGPRCSL
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DGKLDAYVSYSDCEDRKFVNFILKPOLERRGKYLIDPDLIRAPESADLLNL
SCRRLIYVLSDAFLSRAMCSHFREGICRLLELTRRPIETFEQORDDPAIPALRL
ROHRLVLLLMRPGSVTPSSDPKVEYOLALPRKYRPVEDDPOTLODDKDPMLIL
RGRVREGALDSEVNDPDEPDGLGVGPPFGEPSAPPHISGVLSGSRSEVDVSDLSG
RNYKARIDPFLYLSKDDM"

BASE COUNT 329 a 556 c 510 g 300 t
ORIGIN

Query Match 100.0% Score 1233; DB 9; Length 1695;
Best Local Similarity 100.0% Pred. No. 1.1e-178;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAGGTGTCTGTGATAGGGCCCTGACTTCCTCCCGCTGGAAGCAGGTGCTG 60
DB 227 ATGCCAGGTGTCTGTGATAGGGCCCTGACTTCCTCCCGCTGGAAGCAGGTGCTG 286
QY 61 AGGCTGCTTGGGAGCTCAAGTGGCTGGAATGCACGCGTTGGTAGTCTCTGGGCC 120
DB 287 AGGCTGCTTGGGAGCTCAAGTGGCTGGAATGCACGCGTTGGTAGTCTCTGGGCC 346
QY 121 CACTGCTCCCTGCTCACTCCAGTGGCGAAGAGCGGCTCCATTGGGAATTGGGGCC 180
DB 347 CACTGCTCCCTGCTCACTCCAGTGGCGAAGAGCGGCTCCATTGGGAATTGGGGCC 406
QY 181 CACTACAGCCTCCAGAGTACTCTGGGTCAAGGCAACCTGTCAAGAGTGGTGTGCTC 240
DB 407 CACTACAGCCTCCAGAGTACTCTGGGTCAAGGCAACCTGTCAAGAGTGGTGTGCTC 466
QY 241 AGTGTCTTGGGGGTCAAGTGAACCACTGAAGTATAGGGGCTTCACTGCTCCATC 300
DB 467 AGTGTCTTGGGGGTCAAGTGAACCACTGAAGTATAGGGGCTTCACTGCTCCATC 526
QY 301 CAGAACATCAGCTTCCTCTCACTCTTCAGAGAGCGGCGCTCAAGCCACGCGGCT 360
DB 527 CAGAACATCAGCTTCCTCTCACTCTTCAGAGAGCGGCGCTCAAGCCACGCGGCT 586

QY 361 GCGGTGCTGGCCCTCCCTCTGCTGCTGAGCCCTGCTGCTGGCCGCTGCTATATGTC 420
DB 587 GCGGTGCTGGCCCTCCCTCTGCTGCTGAGCCCTGCTGCTGGCCGCTGCTATATGTC 646
QY 421 AAGTGGCTGCTCAAGTGTGCTGCTGTACGAGACGCTATGGGAGTGGAGATTAAC 480
DB 647 AAGTGGCTGCTCAAGTGTGCTGCTGTACGAGACGCTATGGGAGTGGAGATTAAC 706
QY 481 GAGCGGAACCTCTACAGACCTACAGTCTCTCAAGAGATGGCCCGAGAGCCGAATTTC 540
DB 707 GAGCGGAACCTCTACAGACCTACAGTCTCTCAAGAGATGGCCCGAGAGCCGAATTTC 766
QY 541 GTGAACCTTCACTAAAGCCGAGCTGAGACGCGCTGCGGGCTAGAAAGCTTCTCTGAC 600
DB 767 GTGAACCTTCACTAAAGCCGAGCTGAGACGCGCGTGGGGCTTCTCTGAGAC 826
QY 601 GACCGGACCTCTCTGCGCGGCTGAGCCCTCGCGGACCTTGGTGAACCTGACCGCC 660
DB 827 GACCGGACCTCTCTGCGCGGCTGAGCCCTCGCGGACCTTGGTGAACCTGACCGCC 886
QY 661 TGCAGAGCCTCATGCTGCTGCTTTGAGAGCGCCTTCCTGAGCGGGGCTGTCAGACCC 720
DB 887 TGCAGAGCCTCATGCTGCTGCTTTGAGAGCGCCTTCCTGAGCGGGGCTGTCAGACCC 946
QY 721 AGCTTCCGGGAGGCGCTGTGCGGCTGCTGAGCTCACCCGAGACCATCTTCATCAC 780
DB 947 AGCTTCCGGGAGGCGCTGTGCGGCTGCTGAGCTCACCCGAGACCATCTTCATCAC 1006
QY 781 TTGAGAGGCGCAGAGCGGACCCCGGACCCGCGGCTCGGCTGCTGCGGACGACCGC 840
DB 1007 TTGAGAGGCGCAGAGCGGCGCACCCCGGCGCTCGGCTGCTGCGGACGACCGC 1066
QY 841 CACCTGTGACCTGTGCTGCTGAGAGCGCGGCTCGTACCTCTCCGATTTTGG 900
DB 1067 CACCTGTGACCTGTGCTGCTGAGAGCGCGGCTCGTACCTCTCTCCGATTTTGG 1126
QY 901 AAAGAAGTCACTGCGCTGCGCGGAAGGTGCGGTACAGGCGCGGTGGAAGAGACCCC 960
DB 1127 AAAGAAGTCACTGCGCTGCGCGGGAAGGTGCGGTACAGGCGCGGTGGAAGAGACCCC 1186
QY 961 CAGAGCAGCTGACGAGACGACAAAGACCCCATGCTGATTTCTTGAAGCGGAGTCCCTGAG 1020
DB 1187 CAGAGCAGCTGACGAGACGACAAAGACCCCATGCTGATTTCTTGAAGCGGAGTCCCTGAG 1246
QY 1021 GGCGGGGCGCTGAGTCAAGAGGTGAGCCCGGACCTCGAGAGGCGACTGGGTGCGGGGG 1080
DB 1247 GGCGGGGCGCTGAGTCAAGAGGTGAGCCCGGACCTCGAGAGGCGACTGGGTGCGGGGG 1306
QY 1081 CCTGTTTTGAGAGGACCATCACTCACCGACACACAGTGGGGTCTCGCTGGAGAGAGC 1140
DB 1307 CCTGTTTTGAGAGGACCATCACTCACCGACACACAGTGGGGTCTCGCTGGAGAGAGC 1366
QY 1141 CGGAGCAGCGAAGTGGAGCTTCGATCTCGGCTGCGGAACTACAGTCCCGGACAGAC 1200
DB 1367 CGGAGCAGCGAAGTGGAGCTTCGATCTCGGCTGCGGAACTACAGTCCCGGACAGAC 1426
QY 1201 TTCTACTGCTGGTGTCCAAAGATGATATAG 1233
DB 1427 TTCTACTGCTGGTGTCCAAAGATGATATAG 1459

RESULT 3
AX058610
LOCUS AX058610 1659 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 17 from Patent W00075321.
ACCESSION AX058610
VERSION AX058610.1 GI:12310952
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1659)

ATTNORS	Shimkels, R.A., Fernandes, E., Herman, J. and Vernet, C.
TITLE	Polynucleotides and membrane-bound polypeptides encoded thereby
JOURNAL	Patent: WO 0075321-A 17 14-DEC-2000; Curagen Corporation (US)
FEATURES	Location/Qualifiers
source	1. 1659

CDS

BASE COUNT	296 a	551 c	504 g	308 t
GIN				

Query Match	99.98%	Score 1231.4;	DB 6;	Length 1659;
Best Local Similarity	99.98%	Pred. No. 1.9e-178;		
Matches 1232;	Conservative	0;	Mismatches 1;	Indels 0;

Db	904	TGCGAGACGGCTCATCGTGGTGGCTTTGGAGACCCCTTCTTGAGCCGGGGCTGGTGCACGCC	963
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Db	964	AGCTTCGGGAGGAGGCGCTGGGCGGCTGGTGGAGCTCACCGCAGACCCATCTTCATCACG	1023
QY	781	TTGAGAGGCGCAGAGGCGGAGCCCGCGACCCGGCGCTCCGACTGCTGGCAGCACGCG	840
Db	1024	TTGAGAGGCGCAGAGGCGGAGCCCGCGACCCGGCGCTCCGACTGCTGGCAGCACGCGC	1083
QY	841	CACCTGGTAGACCTGCTGCTCTGGAGGGCCGCGCTGACTCCTTCCTCCGATTTTTGG	900
Db	1084	CACCTGGTAGACCTGCTGCTCTGGAGGGCCGCGCTGACTCCTTCCTCCGATTTTTGG	1143
QY	901	AAAGAAATGACAGTGGCGCTGCCGCGGAAGTGGGGTACAGAGCGCGGTGAAGAGACCCC	960
Db	1144	AAAGAAATGACAGTGGCGCTGCCGCGGAAGTGGGGTACAGAGCGCGGTGAAGAGACCCC	1203
QY	961	CAACACGAGTGGAGGAGACACAAAGAACCCATGTCGTGATTTCTGAGAGCGAGTCCCTGAG	1020
Db	1204	CAGACGAGTGGAGGAGACACAAAGAACCCATGTCGTGATTTCTGAGAGCGAGTCCCTGAG	1263
QY	1021	GGCGGGGCGCTGGAGTCAAGTGGAGCCCGGAGCCCTAGAGGGCACTGGGTGGTCGGGGG	1080
Db	1264	GGCGGGGCGCTGGAGTCAAGTGGAGCCCGGAGCCCTAGAGGGCACTGGGTGGTCGGGGG	1323
QY	1081	CCGCTTTTGGAGAGCGATCAAGTCCACCGACACACAGTGGGTCTGCTGGGAGAGAGAC	1140
Db	1324	CCGCTTTTGGAGAGCGATCAAGTCCACCGACACACAGTGGGTCTGCTGGGAGAGAGAC	1383
QY	1141	CGGAGCAGCGAAGTGGAGCTCTCGGATTCGGGCTCGCGAAATCTACAGTGGCGCGACAGC	1200
Db	1384	CGGAGCAGCGAAGTGGAGCTCTCGGATTCGGGCTCGCGAAATCTACAGTGGCGCGACAGC	1443
QY	1201	TTCTACTGCGTGGTGTCCAAAGATGATTTAG 1233	
Db	1444	TTCTACTGCGTGGTGTCCAAAGATGATTTAG 1476	

RESULT 4
AY201368

LOCUS	AX201368	1649 bp	DNA	linear	PAT 30-AUG-2001
DEFINITION	Sequence 47 from Patent WO0153486.				

VERSION	AX201368.1	GI:15391178
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
	1 (bases 1 to 1645)	

TITLE	Compositions and methods for the treatment of tumour
JOURNAL	Patent: WO 0153486-A 47 26-JUL-2001;
FEATURES	Genentech, Inc. (US)
	Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ORIGIN

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Best Local Similarity	99.8%	Pred. No. 3.9e-154		
Matches 1073	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

QY 1 ATGCCAGGTGCTGTATATAGGCCCCCTGACTTCCTCTCCCGCTGTGAAGACCAGGTGCTG 60
104 ATGCCAGGTGCTGTATATAGGCCCCCTGACTTCCTCTCCCGCTGTGAAGACCAGGTGCTG 163

LOCUS	DEFINITION	Mus musculus, similar to single Ig IL-1R-related protein, clone
61	AGGCGTGGCTGGGAGCTCAGTGGCTGTGAACCTACAGGCTGGGTGGTGTCTGGGGCC	120
154	AGGCGTGGCTGGGAGCTCAGTGGCTGTGAACCTACAGGCTGGGTGGTGTCTGGGGCC	223
121	CACCTGCTCCCTGCTTCAGTCCAGTGGCTGAAAGACGGGCTTCCATTTGGAATTGGGGCC	180
224	CACCTGCTCCCTGCTTCAGTCCAGTGGCTGAAAGACGGGCTTCCATTTGGAATTGGGGCC	283
181	CACCTACGCTTCACAGGACTCTGGGCTCAAGGCCAACCTGTCCAGAGGTGCTGTGTCC	240
284	CACCTACGCTTCACAGGACTCTGGGCTCAAGGCCAACCTGTCCAGAGGTGCTGTGTCC	343
241	AGTGTCCGGGGGTCACAGTGAACGACACTGAAGTCTATTGGGGCTTCACTGCTCCATTC	300
344	AGTGTCCGGGGGTCACAGTGAACGACACTGAAGTCTATTGGGGCTTCACTGCTCCATTC	403
301	CAGAACATCAGCTTCCTCTCTCACTCTTCAAGAGGTGGGCTCCACAAAGCCAGCTGGCT	360
404	CAGAACATCAGCTTCCTCTCTCTCACTCTTCAAGAGGTGGGCTCCACAAAGCCAGCTGGCT	463
351	GGGCTGTGGGCTCCCTCCCTGGTCCCTGGTGGCCCTGCTGCTGGCCGCCCTGCTATGTC	420
464	GGGCTGTGGGCTCCCTCCCTGGTCCCTGGTGGCCCTGCTGCTGGCCGCCCTGCTATGTC	523
421	AAAGTCCGCTTCACAGTCTGCTGTGGTACCAAGACCGGCTATTGGGAGGTGGAGATAAAC	480
524	AAAGTCCGCTTCACAGTCTGCTGTGGTACCAAGACCGGCTATTGGGAGGTGGAGATAAAC	583
481	GACGGGAAGCTCTACAGAGCTACGTCCTCAACAGGACTCCCGAGGACCGCAAGTTC	540
584	GACGGGAAGCTCTACAGAGCTACGTCCTCAACAGGACTCCCGAGGACCGCAAGTTC	643
541	GTGAATCTCATCTCAAAAGCCGAGCTGGAGGGGCTCCGGGCTACAACTCTTCTTGAC	600
644	GTGAATCTCATCTCAAAAGCCGAGCTGGAGGGGCTCCGGGCTACAACTCTTCTTGAC	703
601	GACCGCGACCTTCGCGCGGCTGAGAGCCCTCCGCGACCTTGTGTGAACCTGAGCCGC	660
704	GACCGCGACCTTCGCGCGGCTGAGAGCCCTCCGCGACCTTGTGTGAACCTGAGCCGC	763
661	TGCCGAGCCCTCATGCTGTGTGCTTCCGAGAGCGCTTCCAGAGCCGGGCTTGAGGACGAC	720
764	TGCCGAGCCCTCATGCTGTGTGCTTCCGAGAGCGCTTCCAGAGCCGGGCTTGAGGACGAC	823
721	AGCTTCGCGGAGAGGCTTGGCGGCTGTGTGAGCTCACCCGACAGCCCATCTTCATCAC	780
824	AGCTTCGCGGAGAGGCTTGGCGGCTGTGTGAGCTCACCCGACAGCCCATCTTCATCAC	883
781	TTTGAAGGCGACAGGCGGACCCCGCGACCCCGGCGCTCCGCTGCTGCGCCAGCACCGC	840
884	TTTGAAGGCGACAGGCGGACCCCGCGACCCCGGCGCTCCGCTGCTGCGCCAGCACCGC	943
841	CACCTGTGACCTTCCTGCTGTGAGAGGCGGCTCCGAGACTCTTCTCCGATTTTGG	900
944	CACCTGTGACCTTCCTGCTGTGAGAGGCGGCTCCGAGACTCTTCTCCGATTTTGG	1003
901	AAAGAGTGCAGAGTGGGCTCCCGCGGAAAGTGGCGGTACAGAGCCGCTGGAAGAGACCCC	960
1004	AAAGAGTGCAGAGTGGGCTCCCGCGGAAAGTGGCGGTACAGAGCCGCTGGAAGAGACCCC	1063
961	CAGACGACGCTGCAGAGGACAAAGGACCCCATGCTGATTTCTTGAAGGCGGATCCCTGAG	1020
1064	CAGACGACGCTGCAGAGGACAAAGGACCCCATGCTGATTTCTTGAAGGCGGATCCCTGAG	1123
1021	GGCGGGGCTTGGAGATCAGAGTGGACCCCGAACCTGAGAGGCGGACCTGGGTGTC	1075
1124	GGCGGGGCTTGGAGATCAGAGTGGACCCCGAACCTGAGAGGCGGACCTGGGTGTC	1178

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
MGC:18899	IMAGE:4240425	mRNA, complete cds.		
BC010806				
BC010806.1	GI:14789848			
MGC.				
house mouse.				
Mus musculus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
1 (bases 1 to 1568)				
Strausberg, R.				
Direct Submission				
Submitted (12-JUL-2001)				
National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
NIH-MGC Project URL: http://mgc.nci.nih.gov				
Contact: MGC help desk				
Email: gcgaps-remail.nih.gov				
Tissue Procurement: Jeffrey E. Green, M.D.				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305				
Web site: http://www-shgc.stanford.edu				
Contact: (Dickson, Mark) mdcpaxil@stanford.edu				
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov				
Series: IRAX Plate: 25 Row: P Column: 10				
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.				
Location/Qualifiers				
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/db_xref="taxon:10090"				
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/tissue.type="Kidney, normal. 5 month old male mouse."				
/clone.lib="NCI CGAP_Kid14"				
/lab_host="DH10B"				
/note="Vector: pcwv-SPORT6"				
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/codon_start=1				
/product="Similar to single Ig IL-1R-related protein"				
/protein_id="AAH10806.1"				
/db_xref="GI:14789849"				
/translation="MAGVCQMAPNFELSPSDQALGLAREVALNCTAWFSPRQCPQPSYQMLKDGALGNGSHVLEHDFVANSSEIYSVLNLTNAEDYGFYTSYVWYSSHFETLRAGPAGHVAALFASLIVLIVLALVLYALYKRMILMAYODHYGEVENDGKLVDAVSYSDCEDERKFNFTILKPOLERROCKFLPEBDDILPAEPADLIYNLSRCRLIYVLDAPFLSRPWCOSFREGICRLLELTRRPIFTTBEOQRKEPIHPLRLRLQHRILVILVMKPEGVPSDDFWKELOLAPRKVYVPFEDPQTRQDDKDEPLVLRGRAAQGGMSELDPPDEGDLGVNGVPYGEPPPILOETRICIGSHSESDVSDLSGRNYSARPTDFYCLYSEDDV"				
BASE COUNT	359 a	433 c	431 g	345 t
ORIGIN				
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Best Local Similarity	81.7%	Pred. No. 6.5e-122;		
Matches 1007;	Conservative %	0;	Mismatches 223;	Indels 3;
			Gaps	1;
1	ATGCCAGTGTCTGTGATGAGAGGCCCCCTACCTTCCCTCCCGCTGGAAGACAGCTGCTG	60		
Db	ATGGAGAGTGTCTGTGATGATGAGGCCCCCTAATTTCTTCCATCTTGAAGACAGGCTT	179		
QY	AGGCGTGCCTTGGGACAGCTACGTGCTGTGAATGACAGCGCTTGAGTCTTGAGGCC	120		
1				
Db	GCTCTGCCCCTTGGCAGAGAACTTCTTGAATTCACACGCTTGCGTCTCTAGAGCC	239		
QY	CACCTCTCCCTGACCTTCACTGATGAGTGAAGAAGCGGGCTTCCATTTGGAAATTGGGGCC	180		
1				

Db 240 CAGTGTCCCGCCATCAGTGGTGGTGAAGAATGGTGTGGCATTTGGGCATTCGAAGC 299
 Oy 181 CACACAGCCTTCAGAGAGTACCTGGGGTCAAGGCCAACCTGTACAGAGTGTGTGCC 240
 Db 300 CACTTACGCTCCATGAGAGACTTGTGGTACAGGCCAACCTTCTCAGA---GATTGTGCC 356
 Oy 241 AGTGTCTGGGGGTCAACGTGACACGACACTGAATGTATGGGGCTTCACTGCTCCATC 300
 Db 357 AGTGTCTGGGTCAACGTGACCAATGACAGAGACTGTGAACCTTCACTGCTGTGC 416
 Oy 301 CAGAACATCAGTCT 360
 Db 417 TGGAAATCAGCTCCATCT 476
 Oy 361 GCGGTGTGCT 420
 Db 477 GCACTACTGCT 536
 Oy 421 AAGTGTCT 480
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 Oy 481 GAGGGAAGCTCTACAGAGCCTACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
 Db 597 GATGGAGATTTATACAGTCT 656
 Oy 541 GTGAATCTTCT 600
 Db 657 GTAAATTTTCT 716
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 Oy 661 TGCGAGCCT 720
 Db 777 TGTCGGGCT 836
 Oy 721 AGCTTCGGGAGGAGCTGTGGGCTGTGGAGCTGTGGAGCTGTGGAGCTGTGGAGCTGTGG 780
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 VERSION AF239957.1 GI:7271942
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 1421)
 Poltorak, A. and Beutler, B.
 Molecular cloning of mouse SIGIRR, an orphan receptor with a
 Toll-like cytoplasmic domain
 Unpublished
 2 (bases 1 to 1421)
 Poltorak, A. and Beutler, B.
 Direct Submission
 Submitted (01-MAR-2000) Internal Medicine, UT Southwestern Medical
 Center/HMUT, 5323 Harry Hines Boulevard, Dallas, TX 75335-9050, USA
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 Matches 1004; Conservative 0; Mismatches 225; Indels 3; Gaps 1;

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AF113795	1	GI:6714887	Euarchyot; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 1540)
TITLE	Penton-RoL-G., Polentarutti,N., Muzio,M. and Mantovani,A.
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 1540)
AUTHORS	Penton-RoL-G., Polentarutti,N., Muzio,M. and Mantovani,A.
TITLE	Direct Submission
JOURNAL	Submitted (14-DEC-1998) Immunology, Mario Negri Institute, Via Erlarea 62, Milano, MI I-20152, Italy
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Dd	175 GGTCTTGCCCTTGGCAGAGAAGTGTCTTGAATTGCACAGCTGGCTTCTCTAAGCCC 234
Oy	121 CAGTCTCTCCCTGCTTCAGTCCAGTGGCTGAAGAAGCGGCTTCATTGGAAATGGGGCC 180
Dd	235 CAGTGTCCCCCAGCCATCAGTGTGAGTGGCTGAAGAAGTGGCTGGCCAAATGGAAGC 294
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Oy	301 CAGAACATCAGCTTCTCTCTCTTCACTCTTCAAGAGAGCTGGCCCTTAACAAGCCAGTGGCT 360
Dd	412 TGGATATGATGCCCATCTCTTCACTCTTGGGACCGCCGCTGTGGGCATGTGGCT 471
Oy	361 GCGGTGCGGCTCTCCCTCTGGTCTGTGCTGGCCCTGCTGCTGGCCGCTCTATATTC 420
Dd	472 GCAGTAGTGGCTCTCCCTCTGGTCTGTGCTGGCTGGCTGGCTCTCTATATT 531
Oy	421 AAGTCCCTTCAACGTCTGCTGTGATACCAAGAGCGGTATGGAGGTGAGATAAAC 480
Dd	532 AAGTGTGGGTGAACATCTCTGTTGGATACCAAGACACTTACCGGAGGTGGAATGAAC 591
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DB 21337 GAGGGCAGAGGGGTGAGCCATACACCTGTCTCGGCTCTGTGGCCAGCACGCCAC 21396
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ACCESSION AC108908

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 house mouse
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 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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 1 (bases 1 to 61326)
 AUTHORS
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE
 Mus musculus, clone RP23-179K7
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 61326)
 AUTHORS
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Brown, A., Barna, N., Bastien, V., Boguslavsky, L., Bouckgatter, B.,
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 Direct Submission
 Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE JOURNAL COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center Project name: L19209
 Center clone name: 179_K7

 * NOTE: This record contains 78 individual
 * sequencing reads that have not been assembled into
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 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
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QY 383 TCCT 386
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VERSION AF429315.1 GI:17646244
KEYWORDS human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S.,
Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A.,
Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is
associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
TITLE
JOURNAL MEDLINE 21583737
PUBMED 11694876
REFERENCE
AUTHORS Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
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/note="JPH3"
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/gene="JPH3"
/note="component of the junctional complex between plasma
membrane and endoplasmic reticulum"
/codon_start=1
/product="Junctophilin 3"
/protein_id="AAL40941.1"
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BASE COUNT 29056 a 32731 c 30696 g 28283 t 4254 others
ORIGIN

Query Match 5.5%; Score 68; DB 9; Length 125020;
Best Local Similarity 12.2%; Pred. No. 0.11;
Matches 104; Conservative 370; Mismatches 377; Indels 4; Gaps 3;
QY 375 CCCTCTGTCCTCTGACGCTGTCGTCGGCGCCGCTGTATGTCAGTGCCTCA 434
Db 16877 MMKSHGRRRMCTCYSSMMBSMSYSYKMHMSBSGCMHBKCMTMSCCSMYKSS 16936
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Db 16937 WMSSWMCMCMGRRSRKWMYSRGMSRSKSMRYTGSKSMRSMCTSSCYASMCMMC 16996
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QY 555 AAAGCCGAGCTGAGAGGCGTGGGGGCTAACAGCTCTTCTGAGAGCAGCGACCTCT 614

Db 17057 SSSSSCKRGGGSGWKGKGRKSYGRKTRKRSKMKMGAKWYMYRRSRMKMKMYSKRM 17116
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 Db 17177 SKTCMRSTTSTGCGCCCTTTTCCCCCNANTGGGAGACTTTNNKNTYVYKRRNGC 17236
 QY 734 GCGCTGCGCGCTGTGAGCTCAGCCGACGAGACCCATCTTCAATCACTTCCGAGGCGCAG 792
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 Db 17297 YMKMSMSWMSCTYMKCMCKMCKMCKMCKMCKMCKMCKMCKMCKMCKMCKMCKMCK 17356
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 QY 912 GCTGCGCGCTGCGCGCGAGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
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 QY 1032 GAGCTCAGAGGTGAGCGCGCGCGCGCTGAGAGCG-CACTGCTGCTGCTGCTGCTGCT 1090
 Db 17537 MSYKRRKRSYSMCTCRGMSRMSRMSRMSRMSRMSRMSRMSRMSRMSRMSRMSR 17596
 QY 1091 GAGACCCATCAGCTCCACCGCACCGAGTGGGCTCTGCTGAGAGAGCGCGAGAGCG 1150
 Db 17597 TGGMMRSKYYCTGRRMMNTTCCCKRRSYTYRMSAMGRKSSWGMMSASASR 17656
 QY 1151 AAGTGAAGCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1210
 Db 17657 RCKSASRSSWCSRMKMRSSCKMSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMS 17716
 QY 1211 TGGTGTCCAGGATG 1225
 Db 17717 RGRKRSMTKSGSKG 17731
 RESULT 13
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 Sequence split into 4 fragments LOCUS AC091454 Accession AC091454
 Fragment Name Begin End
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 AC091454_1 100001 210000
 AC091454_2 200001 310000
 AC091454_3 300001 394326
 Continuation (3 of 4) of AC091454 from base 200001 (AC091454 Mus musculus chromosome X
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 Best Local Similarity 45.6%; Pred. No 0.27;
 Matches 231; Conservative 0; Mismatches 276; Indels 0; Gaps 0;
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 QY 475 ATAAACGACGAGGAGCTCTGACAGGCTTACGTCTTACAGGACTGCCCGGAGGAGACCGC 534

Db 68819 CTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 68878
 QY 535 AAGTGTGAAGCTTATCTTAAAGCCGACGTGAGAGCGGCTGAGGAGCTTCAAGACTTTC 594
 Db 68879 CTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 68938
 QY 595 CTGGAAGACGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
 Db 68939 CTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 68998
 QY 655 AACCGTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714
 Db 68999 CTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 69058
 QY 715 AACCAACCTTCGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
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 QY 775 ATCACTTCGAGGCGCAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 834
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 AC105364
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 AC105364
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 AC105364.1 GI:18042282
 VERSION
 KEYWORDS
 HTG; PHASE2.
 SOURCE
 Oryza sativa.
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriaraloideae; Oryzoideae; Oryza.
 REFERENCE
 1 (bases 1 to 145936)
 Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
 Saski,C., Henry,D., Oates,R. and Simmons,J.
 Rice Genomic Sequence
 Unpublished
 2 (bases 1 to 145936)
 Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
 Saski,C., Henry,D., Oates,R. and Simmons,J.
 Direct Submission
 Submitted (03-JAN-2002) Clemson University Genomics Institute,
 Clemson University, 100 Jordan Hall, Clemson, SC 29634 USA
 NOTE: This is a 'working draft' sequence. It currently
 consists of 13 contigs. Gaps between the contigs
 are represented as runs of N. The order of the pieces
 is believed to be correct as given, however the sizes
 of the gaps between them are based on estimates that have
 been provided by the submitter.
 This sequence will be replaced
 by the finished sequence as soon as it is available and
 the accession number will be preserved.
 1
 7521: contig of 7521 bp in length
 7522 10885: contig of 3364 bp in length
 10886 13249: contig of 2364 bp in length
 13250 14250: contig of 1001 bp in length
 14251 15828: contig of 1578 bp in length
 15829 32112: contig of 16284 bp in length
 32113 34467: contig of 2355 bp in length

Fri Nov 8 09:52:55 2002

us-09-598-443-1.rge

Page 16

[illegible]

Search completed: November 7, 2002, 18:25:52
Job time : 2663 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:15:50 ; Search time 207 Seconds
(without alignments)
10226.838 Million cell updates/sec

Title: US-09-598-443-1

Perfect score: 1 atgccaggtgtctgtatag.....tgcacaagatgatatgtag 1233

Scoring table: IDENTITY NUC
Gapop 10.0, Gapept 1.0

Seq: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	100.0	1233	20	AAx88091
2	1231.4	99.9	1639	22	AAx27859
3	1029.4	83.5	1428	22	AAx27325
4	1029.4	83.5	1428	22	AAx63958
5	1029.4	83.5	1442	22	AAx63889
6	1025	83.1	1296	21	AAx18292
7	506.4	41.1	851	22	AAx99795
8	245.4	19.9	249	21	AAx06025
9	161.6	13.1	266	22	AAx61892

C	10	69.8	5.7	259	22	AAx53693
C	11	56.4	4.6	799	19	AAx55831
C	12	56.4	4.6	1926	21	AAx50254
C	13	56.4	4.6	1926	22	AAx62902
C	14	56.4	4.6	2580	21	AAx75454
C	15	56.4	4.6	5452	20	AAx90923
C	16	56.4	4.6	8705	20	AAx23778
C	17	56.4	4.6	9600	19	AAx21683
C	18	56.4	4.6	10380	20	AAx22248
C	19	56.4	4.6	10596	14	AAx51731
C	20	56.4	4.6	10596	17	AAx40348
C	21	56.4	4.6	10596	20	AAx15650
C	22	56.4	4.6	16080	21	AAx59553
C	23	54.6	4.4	1925	20	AAx90924
C	24	54.6	4.4	10732	21	AAx10594
C	25	53.4	4.3	3489	21	AAx30290
C	26	53.4	4.3	3489	22	AAx82901
C	27	53.4	4.3	32207	20	AAx73805
C	28	53.4	4.3	137507	19	AAx19941
C	29	52.2	4.2	77536	21	AAx14651
C	30	51.8	4.2	782	22	AAx84576
C	31	50.6	4.1	9045	22	AAx06332
C	32	50.6	4.1	11389	22	AAx59825
C	33	50.6	4.1	58857	21	AAx58471
C	34	50.2	4.1	1833	23	ABx12159
C	35	50.2	4.1	29879	14	AAx46806
C	36	50	4.1	1059	23	AAx54240
C	37	49.8	4.0	1173	20	AAx06679
C	38	49.8	4.0	1173	24	AAx26296
C	39	49.8	4.0	1173	24	AAx26309
C	40	49.8	4.0	1316	22	AAx33452
C	41	49.8	4.0	1394	22	AAx33451
C	42	49.8	4.0	1394	22	AAx33453
C	43	49.8	4.0	1399	22	AAx33236
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C	45	49.8	4.0	2636	22	AAx08044

ALIGNMENTS

RESULT 1	
AAx88091	AAx88091 standard; DNA; 1233 BP.
ID	
AC	AAx88091;
XX	
DT	08-SEP-1999 (first entry)
XX	
DE	Human SIGIRR DNA.
XX	
KW	SIGIRR, anti-inflammatory; anti-autoimmune disease; chromosome 11;
KW	Interleukin-1 receptor; IL1P1.5; arthropod virus multiple congenital;
KW	breast cancer; insulin-dependent diabetes; sickle cell anaemia;
KW	bladder cancer; detection; cell-signal transduction; gene therapy;
KW	immune regulation; cell proliferation; cell death; cell migration;
KW	cell interaction; inflammation; marker; mass spectrometry; human; ss.
OS	Homo sapiens.
XX	
PN	W09932626-A1.
XX	
PD	01-JUL-1999.
XX	
PF	23-DEC-1998; 98WO-US27368.
XX	
PR	23-DEC-1997; 97US-0068770.
XX	
PA	(IMM) IMMUNEX CORP.
XX	
PI	Stims JE;
XX	
DR	WPI; 1999-418925/35.

Murine transport a
Nucleotide sequenc
Epstein Barr virus
EBV tethering prot
Nucleotide sequenc
Anti-sense strand
Vector pshuttle DN
Nucleotide sequenc
Plasmid pcISEBON f
Plasmid pcISEBON f
Nucleotide sequenc
DNA clone pCEC C1.
Epstein Barr Virus
Gene encoding a su
Kaposi's sarcoma-a
Nucleotide sequenc
KSHV LTR DNA (nucl
KSHV long unique c
Nucleotide sequenc
Corn magnesium che
DNA encoding seven
Human novel cytoxi
Nucleotide sequenc
Drosophila melanog
erya region of S.
Pseudomonas aerugi
Human DNAX toll-11
Human DNAX Toll 11
DNA encoding human
DNA encoding human
DNA encoding human
Nucleotide sequenc
Human leucine-rich

DR P-PSDB: AAY25426.
 XX New interleukin-1 receptor analog SIGIRR nucleic acid and proteins
 XX
 PS Claim 1, Page 68-69; 72pp; English.
 XX

This invention describes a novel human SIGIRR DNA, its allelic variants or species homologs which have anti-inflammatory and anti-autoimmune disease activity. SIGIRR is an analog of interleukin-1 receptor. The products of the invention are used (a) as probes or primers for identifying human chromosome 11, to map genes on this chromosome and to identify disease-related genes (particularly in the region 11p15.5 where genes are present associated with e.g. arthropodiposis multiplex congenita, breast cancer, insulin-dependent diabetes, sickle cell anaemia, bladder cancer), including detection of defective genes; (c) to study cell-signal transduction and the SIGIRR system; and (d) in gene therapy. Sense and antisense oligonucleotides can be used to inhibit expression of the SIGIRR gene. The proteins of the invention are used: (1) to study cellular processes (immune regulation, proliferation, death, migration, interaction with other cells and inflammation); (ii) to identify and purify proteins that associate with SIGIRR ligands and receptors, and to measure their biological activity; (iii) in screening for, and rational design of, potential inhibitors of activity; (iv) therapeutically against diseases mediated by SIGIRR polypeptide counter-structures; (v) as molecular weight (m.w.) markers in electrophoresis; (vi) for determining isoelectric points of unknown proteins; (vii) as controls for determining the extent of protein fragmentation (e.g. to aid characterization of protein structures by mass spectrometry); (viii) for generation of antibodies (Ab); (ix) to deliver diagnostic or therapeutic agents to cells that express SIGIRR binding molecules.

XX Sequence 1233 BP; 203 A; 408 C; 380 G; 242 T; 0 other;

Query Match 100.0%; Score 1233; DB 20; Length 1233;
 Best Local Similarity 100.0%; Pred. No. 4.3e-239;
 Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||||
 Db 61 AGGCTGCTTGGGAGCTCAAGTGTGAGTCAAGGCTTGGTATGCTTGGGCC 120
 QY 121 CACTGCTCCCTGCTTCAATGAGTGAAGAGGAGGCTTCAATGGAATTGGGGG 180
 |||||||
 Db 121 CACTGCTCCCTGCTTCAATGAGTGAAGAGGAGGCTTCAATGGAATTGGGGG 180
 QY 121 CACTGCTCCCTGCTTCAATGAGTGAAGAGGAGGCTTCAATGGAATTGGGGG 180
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 Db 121 CACTGCTCCCTGCTTCAATGAGTGAAGAGGAGGCTTCAATGGAATTGGGGG 180
 QY 181 CACTAGAGCTCAGAGTCTGAGTCAAGGCTTCAAGTCAAGAGTCTTGTGTC 240
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 Db 181 CACTAGAGCTCAGAGTCTGAGTCAAGGCTTCAAGTCAAGAGTCTTGTGTC 240
 QY 241 AGTGTCTGGGGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 300
 |||||||
 Db 241 AGTGTCTGGGGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 300
 QY 301 CAGACATCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 |||||||
 Db 301 CAGACATCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 QY 361 GCGGTCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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 Db 361 GCGGTCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 QY 421 AAGTGCCTGCTCAAGTGTGCTGTGATCAAGAGGAGGAGGAGGAGGAGGAGGAG 480
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 QY 481 GAGGGAAGCTCTAGAGGCTTCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 |||||||

Db 481 GAGGGAAGCTCTAGAGGCTTCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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 |||||||
 Db 541 GTGAATCTTATCTTAAGACCGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 601 GACCGGAGCT 660
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 Db 601 GACCGGAGCT 660
 QY 661 TCCGAGGCTTATGAGTGTGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
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 QY 721 ACCTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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 QY 781 TTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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 Db 781 TTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 QY 841 CACCTGAGTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
 |||||||
 Db 841 CACCTGAGTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
 QY 901 AAGAAGTGTACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
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 Db 901 AAGAAGTGTACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 QY 961 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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 QY 1021 GCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
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 QY 1081 CCGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
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 QY 1141 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
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 QY 1201 TTCTACTGCTGTGTGCTTCAAGATGATGTAG 1233
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 Db 1201 TTCTACTGCTGTGTGCTTCAAGATGATGTAG 1233

RESULT 2
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 ID AAF27859 standard; cDNA: 1659 BP.
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 XX AAF27859;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX
 XX Human NOV9 cDNA.
 DE
 XX
 XX Human; NOV9; antiinflammatory; cyostatic; neuroprotective;
 KW cerebrioprotective; immunomodulator; vulnery; vasotrophic; gene therapy;
 KW hyperplasia; tumour; restenosis; psoriasis; Dupuytren's contracture;
 KW diabetes; rheumatoid arthritis; cerebral oedema; Alzheimer's disease; ss.
 OS Homo sapiens.
 XX
 XX MO200075321-A2.
 PN
 XX 14-DEC-2000.
 PD
 XX
 XX 01-JUN-2000; 2000WO-US15303.
 FE

XX 03-JUN-1999: 99US-0137322.
PR 16-MAR-2000: 2000US-0189810.
PR 22-MAR-2000: 2000US-0191158.
PR 30-MAR-2000: 2000US-0193086.
PR 31-MAY-2000: 2000US-0137322.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shinkets Ra, Fernandes E, Herrman J, Vernet C;
XX
XX WPI: 2001-102403/11.
DR P-PSDB: AAB61137.
XX
XX New NOXV polypeptides and polynucleotides, useful in gene therapy, as a
PT diagnostic marker, protein therapeutic, antibody or small molecule drug
PT target for treating immune, proliferative and metabolic diseases and
PT wound healing
XX
XX Laim 8: Page 36-38; 194p; English.
XX
XX The present sequence encodes a new isolated polypeptide (NOXV). The NOXV
CC polypeptides, NOXV nucleic acids, and anti-NOXV antibodies are useful for
CC treating or preventing NOXV-associated disorders. They are also useful
CC for determining the presence of or a predisposition to a disease
CC associated with altered levels of the NOXV polypeptide or nucleic acid.
CC These NOXV-associated disorders include hyperplasias, tumours,
CC stenosis, psoriasis, Dupuytren's contracture, diabetic complications,
CC rheumatoid arthritis, cerebral lesions, diabetic neuropathies, cerebral
CC oedema, senile dementia or Alzheimer's disease. The NOXV polynucleotides
CC are especially useful in gene therapy. Specifically, NOXV is useful as
CC a diagnostic marker or prognostic marker, protein therapeutic and
CC antibody target or small molecule drug target to treat disorders in the
CC immune response pathway, thyroid and metabolic diseases, bone metabolic
CC disorders, diseases of the pancreas (e.g. diabetes or digestive
CC disorders), proliferative diseases, or tissue regeneration and
CC development (e.g. wound healing or treatment of burns).
XX
XX Sequence 1659 BP; 296 A; 551 C; 504 G; 308 T; 0 other:

Query Match 99.9%; Score 1231.4; DB 22; Length 1659;
Best Local Similarity 99.9%; Pred. No. 9.4e-239;
Matches 1332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCAGGTGTCGTGATAGGGGCCCTGACTTCCTCCCGCTGAAGACCGAGTGTG 60
DB 244 ATGCCAGGTGTCGTGATAGGGGCCCTGACTTCCTCCCGCTGAAGACCGAGTGTG 303
QY 61 AGGCGTGCCTTGGGCGAGCTCAAGTGGCTTGAAGTGCACGCGTGGTGTCTCTGGGCC 120
DB 304 AGGCGTGCCTTGGGCGAGCTCAAGTGGCTTGAAGTGCACGCGTGGTGTCTCTGGGCC 363
QY 121 CACTGCTCCCTGCTTCAATCCAGTGGCTGAAGAGCGGCTTCATTTGGGAATGGGGGC 180
DB 364 CACTGCTCCCTGCTTCAATCCAGTGGCTGAAGAGCGGCTTCATTTGGGAATGGGGGC 423
QY 181 CACTACAGCCTCAGAGTACTTCCTGGTCAAGGCGCAAGCTGTCAAGGCTGTGTCC 240
DB 424 CACTACAGCCTCAGAGTACTTCCTGGTCAAGGCGCAAGCTGTCAAGGCTGTGTCC 483
QY 241 AGTGTCTGGGGGTCAAGCTGACACGACTGAAGTCTATGGGGCTTCACTTGTCCATC 300
DB 484 AGTGTCTGGGGGTCAAGCTGACACGACTGAAGTCTATGGGGCTTCACTTGTCCATC 543
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DB 544 CAGAACATCAGCTTCTCTCTTCACTTCAAGAGAGCTGGCCCTTCAAGCCAGTGGCT 603
QY 361 GGGGTGCTGGCTCCCTCTGTGCTGTGGCCCTCTGTGGCCGCGCTGTATGTGTC 420
DB 604 GGGGTGCTGGCTCCCTCTGTGCTGTGGCCCTCTGTGGCCGCGCTGTATGTGTC 663
QY 421 AAGTGCGTCTCAACGTGCTGTGTGTGACAGAGACGCGTATGGGAGGTGAGATTAAC 480

DB 664 AAGTGCGTCTCAACGTGCTGTGTGTGACAGAGACGCGTATGGGAGGTGAGATTAAC 723
QY 481 GACGGAGACTCTAGACGCCCTACGCTCTCTACAGAGACTGCCCGAGAGCGCAAGTTC 540
DB 724 GACGGAGACTCTAGACGCCCTACGCTCTCTACAGAGACTGCCCGAGAGCGCAAGTTC 783
QY 541 GTGAACCTTATCTTAAGCCGAGCTGAGAGCGCGCTGGGGCTTCAAGGCTTCTCTGGAC 600
DB 784 GTGAACCTTATCTTAAGCCGAGCTGAGAGCGCGCTGGGGCTTCAAGGCTTCTCTGGAC 843
QY 601 GACCGGAGCTCTTGGCGCGCTGAGGCCCTCCGCGACTTGGTGAAGCTGAGCCGC 660
DB 844 GACCGGAGCTCTTGGCGCGCTGAGGCCCTCCGCGACTTGGTGAAGCTGAGCCGC 903
QY 661 TGCCAGCGCTCATGTGTGTCTTTGGAGCGCTTCTTACGCCGGGCTGTGTGACGCCAC 720
DB 904 TGCCAGCGCTCATGTGTGTCTTTGGAGCGCTTCTTACGCCGGGCTGTGTGACGCCAC 963
QY 721 AGCTTCGGGAGGCGCTGTGCGGCTGTGAGACTCAACCGCAGACCCATCTTCATCACC 780
DB 964 AGCTTCGGGAGGCGCTGTGCGGCTGTGAGACTCAACCGCAGACCCATCTTCATCACC 1023
QY 781 TTGAGAGGCGCAGAGCGCGACCCCGCACC CGGCTCCGCTGCTGCGCAGACCGCC 840
DB 1024 TTGAGAGGCGCAGAGCGCGACCCCGCACC CGGCTCCGCTGCTGCGCAGACCGCC 1083
QY 841 CACTGTGTACCTTG 900
DB 1084 CACTGTGTACCTTG 1143
QY 901 AAAGAAGTACAGTG 960
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DB 1264 GGGCGGGCCCTGAGTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1323
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DB 1384 CGAGAGCGAGAGTG 1443
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DB 1444 TTCTACTGCTG 1476
RESULT 3
AAS27325
ID AAS27325 standard; cDNA; 1428 BP.
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XX AAS27325;
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XX 07-NOV-2001 (first entry)
XX
XX cDNA encoding novel signal transduction pathway protein, Seq ID 360.
DE
XX
XX Neuroprotective; cytoskeletal; dermatological; immunosuppressive; tumour;
KW anti-inflammatory; anti-HIV; antibacterial; anti-inflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;

KM cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS; ss;
KW acquired immune deficiency syndrome.
XX Homo sapiens.
XX WO200154733-A1.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01312.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
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PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI: 2001-465460/50.
 DR P-PSDB: AAU17408.
 XX

PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders
 PS

Claim 1; SEQ ID No 360; 880bp; English.

XX The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AA52676-AA52785 represent novel signal transduction
 CC pathway protein coding sequences and PCR primers of the invention.
 XX

Query Match 83.5%; Score 1029.4; DB 22; Length 1428;
 Best Local Similarity 99.9%; Pred. No. 4e-198;
 Matches 1030; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 CCTGGTCAAGGCAACCTGTGAGAGTGTGTCAGTGCCTGGGGGTCAACGTGA 262
 DB 196 CCAGGGTCAAGGCCAACCCTGTGAGAGTGTGTCAGTGCCTGGGGGTCAACGTGA 255
 QY 263 CCAGCACTGAACTGTATGGGGCTTCACCTGCTCATCCAGAACATCAGCTTCTCTCT 322
 DB 256 CCAGCACTGAACTGTATGGGGCTTCACCTGCTCATCCAGAACATCAGCTTCTCTCT 315
 QY 323 TCACCTTTAGAGAGTGGCCCTACAGCAGTGGCTGGCTGGCTTCCCTCTCTG 382
 DB 316 TCACCTTTAGAGAGTGGCCCTACAGCAGTGGCTGGCTGGCTTCCCTCTCTG 375
 QY 383 TCCTGCTGCGCTGTGCTGGCGCCCTCTATGTCAGTGCCTGTCACAGGTCTGC 442
 DB 376 TCCTGCTGCGCTGTGCTGGCGCCCTCTATGTCAGTGCCTGTCACAGGTCTGC 435
 QY 443 TCTGTGACAGAGCGGTATGGGAGGTGAGATAAACAGCGGGAAGCTCTACAGACCT 502
 DB 436 TCTGTGACAGAGCGGTATGGGAGGTGAGATAAACAGCGGGAAGCTCTACAGACCT 495
 QY 503 AGCTCTCCACAGCGACTCCCCGAGAGACGAAGTCTGTGAATCTTCACTTAAAGCCGC 562
 DB 496 AGCTCTCCACAGCGACTCCCCGAGAGACGAAGTCTGTGAATCTTCACTTAAAGCCGC 555
 QY 563 AGCTGAGGCGGCTGCGGAGCTACAAGCTTCTGTGAGACGCGGACCTCTGCGCGGCG 622
 DB 556 AGCTGAGGCGGCTGCGGAGCTACAAGCTTCTGTGAGACGCGGACCTCTGCGCGGCG 615
 QY 623 CTGAGCCCTCGCGCAGCTCTTGTGTAACCTGAGCCGCTGCGAGCCCTCATCTGTGTGC 682

DB 616 CTGAGCCCTCGCGCAGCTCTTGTGTAACCTGAGCCGCTGCGAGCCCTCATCTGTGTGC 675
 QY 683 TTTTGGAGCGCTTCCGTGAGACCGGGCCCTGTGACAGCCACAGCTTCCGGGAGGCGCTTGC 742
 DB 676 TTTTGGAGCGCTTCCGTGAGACCGGGCCCTGTGACAGCCACAGCTTCCGGGAGGCGCTTGC 735
 QY 743 GGCTGTGAGCTCAACCCGACAGCCATCTTCATCACTTTCAGAGGCGACAGCGCGACC 802
 DB 736 GGCTGTGAGCTCAACCCGACAGCCATCTTCATCACTTTCAGAGGCGACAGCGCGACC 795
 QY 803 CCGCGACCCGGGCGCTCGCCCTGTGCGGACGACCGGACCGGCTGTGACCTTGTCTCT 862
 DB 796 CCGCGACCCGGGCGCTCGCCCTGTGCGGACGACCGGACCGGCTGTGACCTTGTCTCT 855
 QY 863 GGAGGCGCGGCTCGGACCT 922
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 QY 1223 ATGATATGTAG 1233
 DB 1216 ATGATATGTAG 1226

RESULT 4
 ID AA163958 standard; cDNA; 1428 BP.
 XX
 XX AA163958;
 AC
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 XX
 DT 22-OCT-2001 (first entry)
 XX
 XX Human polynucleotide SEQ ID NO 166.
 DE
 XX Human; antihistaminic; antirheumatic; antiproliferative; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
 KW antiinflammatory; antilucer; vulnary; anticonvulsant; antibacterial;
 KW cardiovascular disorder; gene therapy; cancer; immune disorder;
 KW antiparasitic; neurologic disease; infection; human; ss.
 OS Homo sapiens.
 OS
 PN WO200155308-A2.
 PN
 PD 02-AUG-2001.
 PD
 XX
 PF 17-JAN-2001; 2001WO-0501309.
 PF
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205543.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR XX

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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488781/53.
XX P-PSDB; AAM43652.
XX DR
XX PT New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating and/or preventing human diseases and disorders -
XX Claim 1; SEQ ID NO 166; 664bp + Sequence listing; English.
XX PS
XX XX

CC The invention relates to human polynucleotides (AA163803-AA164012) and
CC the encoded proteins (AA44497-AA44360) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX

Sequence 1428 BP; 288 A; 462 C; 426 G; 250 T; 2 other:
Query Match 83.5%; Score 1029.4; DB 22; Length 1428;
Best Local Similarity 99.9%; Pred. No. 4e-198;
Matches 1030; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 203 CCGGCTCAGAGCCCAACCTGTCAGAGTCTTGTCCAGTGTCTGGGGCTCAACGTGA 262
DB 196 CCAGGGTCAAGGCCCAACCTGTAGAGTGTCTGTCCAGTGTCTGGGGCTCAACGTGA 255
OY 263 CCAGCAGTGAAGTCTATGAGGGGCTTACCTGCTCCATCCAGAACATCAGCTTCTCTCT 322
DB 256 CCAGCAGTGAAGTCTATGAGGGGCTTACCTGCTCCATCCAGAACATCAGCTTCTCTCT 315
OY 323 TCACCTTCAGAGAGCTGGCTTACAGGACGTGGCTGGCTGGCTGGCTGGCTGGCTGG 382
DB 316 TCACCTTCAGAGAGCTGGCTTACAGGACGTGGCTGGCTGGCTGGCTGGCTGGCTGG 375
OY 383 TCTCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 442
DB 376 TCTCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 435
OY 443 TCTGTATCCAGAGACCGCTATGAGGGAGTGAATTAACGACGGGAAGCTCTACGACGCT 502
DB 436 TCTGTATCCAGAGACCGCTATGAGGGAGTGAATTAACGACGGGAAGCTCTACGACGCT 495
OY 503 ACGTCTCAGAGAGAGTGGCCCGGAGACCGCAATGCTGTAATCTCAATCTCAAGCCGC 562
DB 496 ACGTCTCAGAGAGAGTGGCCCGGAGACCGCAATGCTGTAATCTCAATCTCAAGCCGC 555
OY 563 ACGTGGAGGCGGCTGCGGGGCTACAGAGCTTCTCTGAGAGACCGGACGCTCTGCGCGCG 622
DB 556 ACGTGGAGGCGGCTGCGGGGCTACAGAGCTTCTCTGAGAGACCGGACGCTCTGCGCGCG 615
OY 623 CTGAGCCCTCGCGGACGCTTGTGTAACCTGAGCGGCTGCGGACGCTATGCTGTGTC 682
DB 616 CTGAGCCCTCGCGGACGCTTGTGTAACCTGAGCGGCTGCGGACGCTATGCTGTGTC 675
OY 683 TTTGGAGGCGCTTCTGAGCGGGGCTGTGAGCACAAGCTTCCGAGAGGGGCTGTGTC 742
DB 676 TTTGGAGGCGCTTCTGAGCGGGGCTGTGAGCACAAGCTTCCGAGAGGGGCTGTGTC 735
OY 743 GGCCTGCTGAGCTCAACCGGACAGACCATCTTCATCAGCTTTCAGAGGCGCAGAGCGCAG 802
DB 736 GGCCTGCTGAGCTCAACCGGACAGACCATCTTCATCAGCTTTCAGAGGCGCAGAGCGCAG 795
OY 803 CCGGCAACCCGGGCGCTCGGCTGTGCGGACAGCCGACCTGCTGTGACCTTGTGCTCT 862
DB 796 CCGGCAACCCGGGCGCTCGGCTGTGCGGACAGCCGACCTGCTGTGACCTTGTGCTCT 855
OY 863 GGAGGCGCGGCGCTGTGAGTCTCTCTCGATTTTGGAAAAGTGAAGCTGGGGGCTGTC 922
DB 856 GGAGGCGCGGCGCTGTGAGTCTCTCTCGATTTTGGAAAAGTGAAGCTGGGGGCTGTC 915

OY 923 CCGGAGAGTGGCGGTACAGAGCCGGTGGAGAGAGACCCCGACGAGCTGACAGAGACA 982
DB 916 CCGGAGAGTGGCGGTACAGAGCCGGTGGAGAGAGACCCCGACGAGCTGACAGAGACA 975
OY 983 AGGACCCCATGCTGATTTCTTGAAGGCGGAGTCCCTGAGGGCCGGGCTGACCTAGAG 1042
DB 976 AGGACCCCATGCTGATTTCTTGAAGGCGGAGTCCCTGAGGGCCGGGCTGACCTAGAG 1035
OY 1043 TGGACCCCGAGCTGAGGGGCGAGCTGGGTGTCCGGGGGCTTTTGGAGAGCCATCAG 1102
DB 1036 TGGACCCCGAGCTGAGGGGCGAGCTGGGTGTCCGGGGGCTTTTGGAGAGCCATCAG 1095
OY 1103 CTCACCCCGACACAGAGTGGGCTCTGCTGGGAGAGAGCCGAGACGAGTGAAGTCT 1162
DB 1096 CTCACCCCGACACAGAGTGGGCTCTGCTGGGAGAGAGCCGAGACGAGTGAAGTCT 1155
OY 1163 CGGATCTGGGCTGGGGAAGTCACTGCCCCGACAGACTTCTACTGCTGTGTCCAGAG 1222
DB 1156 CGGATCTGGGCTGGGGAAGTCACTGCCCCGACAGACTTCTACTGCTGTGTCCAGAG 1215
OY 1223 ATGATATGTAG 1233
DB 1216 ATGATATGTAG 1226
RESULT 5
AA163889
ID AA163889 standard; cDNA; 1442 BP.
XX
XX AA163889;
AC
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 97.
XX
XX Human; antihypertensive; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antinflammatory; antitumor; vulnary; anticonvulsant; antibacterial;
KW antiparasitic; gardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human; ss.
OS Homo sapiens.
XX
XX
PN WO200155308-A2.
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.

Sequence 1442 BP; 297 A; 465 C; 430 G; 250 T; 0 other;

Query Match 83.5%; Score 1029.4; DB 22; Length 1442;
Best Local Similarity 99.9%; Pred. No. 4e-198;
Matches 1030; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 203 CCTGGGTCAGAGCCCAACCTGTTCAGAGGTGCTTGTCTCAGTGTCTCTGGGGGTCAACGTGA 262
    |||||||
DB 204 CCAGGGTCAGAGCCCAACCTGTTCAGAGGTGCTTGTCTCAGTGTCTCTGGGGGTCAACGTGA 263
QY 263 CCAGACACTGAAGTCTATGAGGGGCTTCACCTGTCTCATTCAGAACTACAGTCTCTCTCT 322
    |||||||
DB 264 CCAGACACTGAAGTCTATGAGGGGCTTCACCTGTCTCATTCAGAACTACAGTCTCTCTCT 323
QY 323 TCACCTCTCAGAGACTGGGCTTCACAGCCAGTGGCTGGGCTGGCTCTCCCTCTGG 382
    |||||||
DB 324 TCACCTCTCAGAGACTGGGCTTCACAGCCAGTGGCTGGGCTGGCTCTCCCTCTGG 383
QY 383 TCCCTGCTGGCCCTGCTGCTGGGCGCCCTGCTCTATGTCAAGTGGCCGTCTCAAGCTGTGC 442
    |||||||
DB 384 TCCCTGCTGGCCCTGCTGCTGGGCGCCCTGCTCTATGTCAAGTGGCCGTCTCAAGCTGTGC 443
QY 443 TCTGTGTACCAAGACCGCGATGAGGGAGGTGAGATTAACGAGCGGAAGCTTACGACGCT 502
    |||||||
DB 444 TCTGTGTACCAAGACCGCGATGAGGGAGGTGAGATTAACGAGCGGAAGCTTACGACGCT 503
QY 503 ACGTCTCTACAGGACGACGTCGCCCGAGAGACCGCAACTGTGTGAATCTTCACTCTAAAGCCGC 562
    |||||||
DB 504 ACGTCTCTACAGGACGACGTCGCCCGAGAGACCGCAACTGTGTGAATCTTCACTCTAAAGCCGC 563
QY 563 AGCTGTGAGCGGCGCTGTCGAGGAGCTTCTCTGAGACGACCGGACCTCTGCGCGCG 622
    |||||||
DB 564 AGCTGTGAGCGGCGCTGTCGAGGAGCTTCTCTGAGACGACCGGACCTCTGCGCGCG 623
QY 623 CTGAGCCCTCCGCGCACTCTTGTGTGAACCTGAGCCGCTCCGACGCTCATCTGTGTGC 682
    |||||||
DB 624 CTGAGCCCTCCGCGCACTCTTGTGTGAACCTGAGCCGCTCCGACGCTCATCTGTGTGC 683
QY 683 TTTGGAGAGGCTTCTGTGAGCGGGGCTGTGAGCACAGCTTCGGGAGGGGCTGTGC 742
    |||||||
DB 684 TTTGGAGAGGCTTCTGTGAGCGGGGCTGTGAGCACAGCTTCGGGAGGGGCTGTGC 743
QY 743 GGCCTCTGAGAGCTCAACCCGAGAACCCATCTTCATCATCTTCAGAGGGGCGAGAGCGCGACC 802
    |||||||
DB 744 GGCCTCTGAGAGCTCAACCCGAGAACCCATCTTCATCATCTTCAGAGGGGCGAGAGCGCGACC 803
QY 803 CCGCGCACCCGGCGCTCCGCGCTGCTGCGCGACAGCCGACCTGTGACCTTGTCTCT 862
    |||||||
DB 804 CCGCGCACCCGGCGCTCCGCGCTGCTGCGCGACAGCCGACCTGTGACCTTGTCTCTCT 863
QY 863 GGAGGCGCGGCTCGTGAATCTTCTCCGATTTTGGAAAGTAAGTGAAGTGAAGTGGGCTGC 922
    |||||||
DB 864 GGAGGCGCGGCTCGTGAATCTTCTCCGATTTTGGAAAGTAAGTGAAGTGAAGTGGGCTGC 923
QY 923 CGCGGAAGGTGCGGTACAGGCGCGGTGGAAGAGACCCCGAGACGAGCTGACGAGACGA 982
    |||||||
DB 924 CGCGGAAGGTGCGGTACAGGCGCGGTGGAAGAGACCCCGAGACGAGCTGACGAGACGA 983
QY 983 AGGACCCCATGCTGATTTCTTTCAGAGCCGAGTCCCTGAGGGGCGGGCCCTGGACTAGAG 1042
    |||||||
DB 984 AGGACCCCATGCTGATTTCTTTCAGAGCCGAGTCCCTGAGGGGCGGGCCCTGGACTAGAG 1043
QY 1043 TGGACCCCGAGACCTGAGGGGCGAGCTGGGCTGGGGGCGGCTTTTGGAGAGCCATAG 1102
    |||||||
DB 1044 TGGACCCCGAGACCTGAGGGGCGAGCTGGGCTGGGGGCGGCTTTTGGAGAGCCATAG 1103
QY 1103 CTCCACCGCACACAGTGGGGTCTGCTGGGAGAGAGCCGAGACGAGCAAGTGAAGCT 1162
    |||||||
DB 1104 CTCCACCGCACACAGTGGGGTCTGCTGGGAGAGAGCCGAGACGAGCAAGTGAAGCT 1163
QY 1163 CGGATCTCTGGGCTCGGAAACTACAGTGGCGCGACAGACTTCTACTGCTGTGTCTCAAG 1222
    |||||||
DB 1164 CGGATCTCTGGGCTCGGAAACTACAGTGGCGCGACAGACTTCTACTGCTGTGTCTCAAG 1223
```

QY 1223 ATGATATGTAG 1233
|||||||
DB 1224 ATGATATGTAG 1234

RESULT 6
AAFI8292
ID AAFI8292 standard; DNA; 1296 BP.

AC AAFI8292;

DT 14-MAR-2001 (first entry)

DE Lung cancer associated polynucleotide sequence SEQ ID 311.

XX Human; lung cancer associated protein; neuroprotective; cytostatic;
XX cardioactive; immunomodulatory; muscular active; vulnerary;
XX gastrointestinal; nephrotoxic; antiinfective; gynecological;
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
XX proliferative disorder; wound healing; infectious disease; ds.

OS Homo sapiens.

PN WO20005180-A2.

PD 21-SEP-2000.

PE 08-MAR-2000; 2000WO-US05918.

PR 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (ROSE/) ROSEN C A.

PI Ruben SM;

DR WPI: 2000-587514/55.

DR P-PSDB: AAB58416.

PT Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX
XX
XX
PS Claim 1; Page 769-770; 1425bp; English.

XX Polynucleotide sequences AAFI7982 - AAFI8424 encode human lung cancer
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer
XX associated proteins and polynucleotide sequences, their agonists, and
XX antagonists may have neuroprotective; cytostatic; cardioactive;
XX immunomodulatory; muscular active general; vulnerary; gastrointestinal
XX general; nephrotoxic; antiinfective; gynecological; or antibacterial
XX activity. The invention also includes antibodies specific for the
XX protein or polynucleotide sequences. The lung cancer associated
XX polynucleotide sequences may be used for detection of lung cancer,
XX chromosome identification, as chromosome markers, and for numerous other
XX diagnostic or research purposes. The proteins may be used to treat
XX disorders such as neural, immune, muscular, reproductive,
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX disorders. The proteins may also be used in the treatment of wounds and
XX infectious diseases. Polynucleotide sequences AAFI8425 - AAFI8433 and
XX peptide AAB58549 are used in the course of the invention for the
XX identification and characterisation of the polynucleotide and protein
XX sequences.

XX Sequence 1296 BP; 242 A; 431 C; 394 G; 227 T; 2 other;

Query Match 83.1%; Score 1025; DB 21; Length 1296;
Best Local Similarity 99.7%; Pred. No. 3e-197;
Matches 1025; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 206 GGGTCAGAGCCCAACCTGTTCAGAGGTGCTTGTCTCAGTGTCTGGGGGTCAACGTGACCA 265
|||||||

Db 67 GGGTCAGAGCCACCTCTCAGAGGTGCTGTGTACAGTCTCCTGGGGGTCAGAGTGACCA 126
QY 266 GCACCTAAGTCTATGAGGCGCTTACCTGCTCATCCAGAACATCAGCTTCTCTCTTCA 325
Db 127 GCACTGAAGTCTATGAGGCGCTTACCTGCTCATCCAGAACATCAGCTTCTCTCTTCA 186
QY 326 CTCTTCAGAGAGTGGCTTACAGCCAGTGGCTGGTGGCTCCCTCTGATCC 385
Db 187 CTCTTCAGAGAGTGGCTTACAGCCAGTGGCTGGTGGCTCCCTCTGATCC 246
QY 386 TGTGAGGCGCTGCTGGCGCCCTGCTATGTCAAGTGGCTTCACAGTGGCTCT 445
Db 247 TGTGAGGCGCTGCTGGCGCCCTGCTATGTCAAGTGGCTTCACAGTGGCTCT 306
QY 446 GGTACCAAGAGCGGTATGAGGAGTGGAGTAAACAGAGCGGAGCTTCAGAGCGCTAG 505
Db 307 GGTACCAAGAGCGGTATGAGGAGTGGAGTAAACAGAGCGGAGCTTCAGAGCGCTAG 366
QY 506 TGTCTACAGAGAGTGGCGCCGAGAGCCAGAGTCTGTGAATTCATCTTAAAGCCGAC 565
Db 367 TGTCTACAGAGAGTGGCGCCGAGAGCCAGAGTCTGTGAATTCATCTTAAAGCCGAC 426
QY 566 TGAAGAGCGCTGGGGCTACAGAGCTCTCTGAGAGAGCGGAGCTCTGCGCGCGCTG 625
Db 427 TGAAGAGCGCGTGGGGCTACAGAGCTCTCTGAGAGAGCGGAGCTCTGCGCGCGCTG 486
QY 626 AGCCCTCGCGGAGCTCTTGTGTAGCTAGCCGCTGCGAGCGCTCATCTGTGTCTTT 685
Db 487 AGCCCTCGCGGAGCTCTTGTGTAGCTAGCCGCTGCGAGCGCTCATCTGTGTCTTT 546
QY 686 CGAGAGCGCTCTCTGAGCGCGGCTGTGTGAGCGAGCTCTGCGAGCGGCTGTGCTCCG 745
Db 547 CGAGAGCGCTCTCTGAGCGCGGCTGTGTGAGCGAGCTCTGCGAGCGGCTGTGCTCCG 606
QY 746 TGTGAGAGCTACAGCGAGAGCCATCTCATACCTTCAGAGGCGAGAGCGGAGCGGCG 805
Db 607 TGTGAGAGCTACAGCGAGAGCCATCTCATACCTTCAGAGGCGAGAGCGGAGCGGCG 666
QY 806 CGCAGCGGCGCTCTGCGCTCTGCGGAGAGAGCCAGCGGAGCTGTGACCTTGTGTGGA 865
Db 667 CGCAGCGGCGCTCTGCGCTCTGCGGAGAGAGCCAGCGGAGCTGTGACCTTGTGTGGA 726
QY 866 GGGCGGCTCTGAGAGCTCTCTCTGATTTTGAAGAGTGTGAGTGGCTGTGCGC 925
Db 727 GGGCGGCTCTGAGAGCTCTCTCTGATTTTGAAGAGTGTGAGTGGCTGTGCGC 786
QY 926 GGAAGTGTGAGAGCGGCTGTGAGAGAGAGCCAGAGCGAGCTGTGAGCTGTGTGGA 985
Db 787 GGAAGTGTGAGAGCGGCTGTGAGAGAGAGCCAGAGCGAGCTGTGAGCGAGAGAG 846
QY 986 ACCCATGCTGATTTCTTCGAGGCGGAGTCCCTGAGAGGCGGCGCTTGGAGCTGAGAGTGG 1045
Db 847 ACCCATGCTGATTTCTTCGAGGCGGAGTCCCTGAGAGGCGGCGCTTGGAGCTGAGAGTGG 906
QY 1046 ACCCGAGCTGTGAGGCGAGCTGTGCTGCGGGGCGCTTTTGGAGAGCCATGAGCTC 1105
Db 907 ACCCGAGCTGTGAGGCGAGCTGTGCTGCGGGGCGCTTTTGGAGAGCCATGAGCTC 966
QY 1106 CACCGCAGCAGTGGGCTCTGCTGGAGAGAGCCGAGAGCAGAGTGTGAGCTGTGCG 1165
Db 967 CACCGCAGCAGTGGGCTCTGCTGGAGAGAGCCGAGAGCAGAGTGTGAGCTGTGCG 1026
QY 1166 ATTCGAGCTGTGAGAGTGTGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1225
Db 1027 ATTCGAGCTGTGAGAGTGTGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1086
QY 1226 ATATGTAG 1233
Db 1087 ATATGTAG 1094

RESULT 7
AAH9795/c

ID XX AAH9795 standard; cDNA; 851 BP.
AC XX AAH9795;
XX 16-OCT-2001 (first entry)
XX Human protein encoding cDNA sequence spq ID NO:630.
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW anti-infective; antineoplastic; antidiabetic; antihypertensive;
KW anti-HIV; fungicide; antitumor; cardiovascular; antineoplastic; anesthetic;
KW antiaggregant; haemostatic; valnerary; antitumor; osteoporosis; eczema;
KW dermatological; antiallergic; antidiabetic; antidiabetic; cytosolic;
KW neuroprotective; antidepressant; neurotrophic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antitumor; antidiabetic; antidiabetic;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autolysis;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX Homo sapiens.
XX WO200153455-A2.
XX 26-JUL-2001.
XX 22-DEC-2000; 2000WO-US35017.
XX 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI WPI: 2001-457603/49.
DR P-PSDB: AAM25854.
XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX Claim 1: Page 653; 1217p; English.
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antineoplastic; antineoplastic;
CC antidiabetic; immunosuppressive; antidiabetic; endocrine; cardiac;
CC central nervous system; vitruide; anti-HIV; fungicide; antitumor;
CC cardiovascular; antineoplastic; antidiabetic; antidiabetic; antidiabetic;
CC antidiabetic; cytosolic; neuroprotective; antidiabetic; antidiabetic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antitumor therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX Sequence 851 BP; 136 A; 273 C; 289 G; 153 T; 0 other;
Query Match 41.1%; Score 506.4; DB 22; Length 851;

Best Local Similarity 99.8%; Pred. No. 5.9e-93;
Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 726 CCGGGAGGGGCTGCGGCTGCTGAGACTCACCACCCAGACCCATTTATACACTTCA 785
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 720 CAGGGAGGGGCTGCGGCTGCTGAGACTCACCACCCAGACCCATTTATACACTTCA 661
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 786 GGGCCAGAGGCGGAGCCCGGCGGCGGCTCCGCTGCTGCGGCGACCGGCGGCT 845
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 660 GGGCCAGAGGCGGAGCCCGGCGGCGGCTCCGCTGCTGCGGCGACCGGCGGCT 601
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 846 GGTGACCTTGTCTGCTGAGAGGCGGCGGCTCCGCTGCTGCGGCGGCGGCT 905
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 600 GGTGACCTTGTCTGCTGAGAGGCGGCGGCTCCGCTGCTGCGGCGGCGGCT 541
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 906 AGTGCAGGCGGCGGCTCCGCGGAGGTGGGTACAGCCGCGGTGAGAGGAGCCCGAGC 965
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 540 AGTGCAGGCGGCGGCTCCGCGGAGGTGGGTACAGCCGCGGTGAGAGGAGCCCGAGC 481
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 966 GCAGCTGAGAGGAGAGGAGCCCATGCTGATTTCTTGAGGCGGAGCTCCGAGGCGG 1025
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 480 GCAGCTGAGAGGAGAGGAGCCCATGCTGATTTCTTGAGGCGGAGCTCCGAGGCGG 421
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1026 GGGCCCTGAGCTGAGAGGTGGAGCCCGGAGCCCTGAGGCGGAGCTGGGCTGCT 1085
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 420 GGGCCCTGAGCTGAGAGGTGGAGCCCGGAGCCCTGAGGCGGAGCTGGGCTGCT 361
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1086 TTTTGGAGGCGCATGAGCTCCAGCCGAGCAGCAGCTGGGCTGCTGGTGGAGAGCCGGAG 1145
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 360 TTTTGGAGGCGCATGAGCTCCAGCCGAGCAGCAGCTGGGCTGCTGGTGGAGAGCCGGAG 301
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1146 CAGCGAAGTGGAGCTGCTGGATCTGCGGCTGCGGAACTGAGTGGCCGAGACTTCTA 1205
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 300 CAGCGAAGTGGAGCTGCTGGATCTGCGGCTGCGGAACTGAGTGGCCGAGACTTCTA 241
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1206 CTGCTGCTGCTCCAGAGTATGATGTAG 1233
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 CTGCTGCTGCTCCAGAGTATGATGTAG 213
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 8
AAC06025
ID AAC06025 standard; cDNA; 249 BP.

XX AAC06025;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 10100.

KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

OS Homo sapiens.

PN EP103401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 9905-0122487.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX

PS Claim 1; SEQ ID 10100; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from
mRNAs encoding secreted proteins. No ORF has yet been conclusively
identified within the present sequence. The 5' ESTs were prepared from
total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
sequences usually correspond mainly to the 3' untranslated region (UTR)
of the mRNA because they are often obtained from oligo-dT primed cDNA
libraries. Such ESTs are not well suited for isolating cDNA sequences
derived from the 5' ends of mRNAs and even in those cases where longer
cDNA sequences have been obtained, the full 5' UTR is rarely included.
5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
in diagnostic, forensic, gene therapy and chromosome mapping procedures.
They are used to obtain upstream regulatory sequences and to design
expression and secretion vectors.

Sequence 249 BP; 43 A; 87 C; 65 G; 54 T; 0 other;

Query Match 19.9%; Score 245.4; DB 21; Length 249;

Best Local Similarity 99.6%; Pred. No. 1.6e-40;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 284 CCTTCACTGCTGCATCCAGAACATCAGCTTCTCCTTCACTCTTCAGAGAGCTGGCC 343
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 CCTTCACTGCTGCATCCAGAACATCAGCTTCTCCTTCACTCTTCAGAGAGCTGGCC 60
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 344 CTACAAAGCCAGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CTACAAAGCCAGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 404 CCGCCCTGCTATGTCAGAGTCCGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 463
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 CCGCCCTGCTATGTCAGAGTCCGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 464 GGGAGGTGAGATTAACGACGCGGAAGCTCTACGAGCCTTCTTCTTACAGCGACTGCC 523
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 GGGAGGTGAGATTAACGACGCGGAAGCTCTACGAGCCTTCTTCTTACAGCGACTGCC 240
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 524 CCGAGGA 530
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 CCGAGGA 247
    1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 9
AAK61892
ID AAK61892 standard; cDNA; 266 BP.

XX AAK61892;

DT 06-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:6952.

KM Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ss.

OS Homo sapiens.

PN WO200157182-A2.

PD 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US01354.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

Df	732	CCCTCCTGTCCTGC6GCCCTCGTCTGTCTGGCCCTCTGTGCTCGTCCCTCTGTGCCCCCTCTG6CCCTTC	673
Oy	665	GACGCCCTCATGCTGTGCTTTTGAGACGCTTCTGTAGACGGGGCTGGTAGCCACAGCT	724
Dd	672	TGCACCCTCTCTGCTGCTGCCCTCTGCTCTGCTCTGCTGCCCTCTGCCCTCTGCTGCCCTTC	613
Oy	725	TCCGGGAGGGGCTGTGCGGCTGTGTAGACTCACCCGAGACCCATCTTATACCTTCG	784
Dd	612	TGCTCTCTGCCCCTCTCTGCTGCTGCTGCCCTCTGCTGCCCTCTGCTGCCCTCTGCTGCC	553
Oy	785	AAGGCCAGAGGGGCGACCCCGGCGACCTGCGCTGCGCTGCGCGACACAGCCAGCC	844
Dd	552	TGCCCTCTCTGCTGCCCTCTCTGCTGCTGCCCTCTCTCTGCTGCTGCCCTCTGCTGCC	493
Oy	845	TGCTGACCTTGTCTGCTGTGAGGCC	870
Dd	492	TCTGCCCCCTCTCTGCTGCTGCC	467
RN	13		
ID	AAFR2902/C		
XX	AAF82902 standard; DNA; 1926 BP.		
AC	AAF82902;		
DE	29-JUN-2001 (first entry)		
DE	EBV tethering protein EBNA1 encoding DNA.		
KW	Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis;		
KW	Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;		
KW	EBV latency-associated nuclear antigen; LANA; EBNA1; ds.		
OS	Epstein-barr virus.		
FT	Key	Location/Qualifiers	
FT	CDS	1..1926	
FT		/*tag= a	
PN	WO200125484-A2.		
PD	12-APR-2001.		
PF	29-SEP-2000; 2000MO-US26908.		
PR	01-OCT-1999; 99US-0410399.		
PI	(JNM1) UNTIV MICHIGAN.		
PI	Robertson ES, Colter MA;		
DR	WPI: 2001-281736/29.		
DR	P-PsDB: AAB62332.		
PT	A composition for use in gene therapy comprises an expression vector		
PT	that includes a nucleic acid sequence encoding a nucleic acid binding		
PT	protein -		
PS	Disclosure: Fig 9C; 60pp: English.		
XX	The invention provides a composition comprising nucleic acid, histone H1		
XX	protein and expression vector operatively encoding a protein suitable		
XX	for tethering the nucleic acid to the histone H1 protein, where the		
XX	tethering protein is LANA. The composition is useful in aiding the		
XX	retention of the viral DNA in the host cell. The viral vector encodes a		
XX	protein suitable for tethering DNA to Histone H1. Methods for screening		
XX	for compounds which are agonistic or antagonistic for the tethering of		
XX	viral proteins to histone H1 and DNA binding sites are useful for		
XX	developing the method of viral transfer. The composition has applications		
XX	to gene therapy, including the treatment of multiple sclerosis,		
XX	Parkinson's disease, Huntington disease and diabetes. The present		
XX	sequence represents the nucleotide sequence of the Epstein-Barr virus		
XX	(EBV) tethering protein ENNA1.		

XX		Sequence	1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other:	
SQ				
		Query Match	4.6%; Score 56.4; DB 22;	Length 1926;
		Best Local Similarity	44.5%;	Pred. No. 0.021;
		Matches 225; Conservative	0; Mismatches 281; Indels	0; Gaps 0;
OY		365	TGCTGGCCCTCCTCGTGTGCTGTGGGCCCTGTGCCTTGAGCGCCCTGCTATATGTCAACT	424
Dd		972	TGCTCTCGGCCCCCTCCGTGCTACGCCCCTTCCTCTCTCTGCGCCCTCCCTCCGCTCCGTC	913
OY		425	GCCGCTCAAGCTGCTGCTGTGTACCAGAGGAGCGCATGGSGAAGSTGGAGATTAACAAGCG	484
Dd		912	TCTCTGCCCTCTGTGCCCCCTCGTGTGTGCCCCCTTCCCTGCCCCCTCTGTCTGTGCCCCCTTC	853
OY		485	GGAAAGCTACTACAGCACGCTAACGTTCTCTACAGAGCATGCCCCGAGGAGACGCAAGTTCTGA	544
Dd		852	TGCCCTCTCTCTCTGCTGCTCTGCCCCCTTCCTGCCCCCTCTCTCTCTCTCTGCCCCCTCTG	793
OY		545	ACTTCATCTCTTAAAGCGCAGCTGAGAGCGCGCTGAGGAGCTACAAAGCTCTTCTGTGACGAC	604
Dd		792	TCTCTGCTCTGCGCCCTCCGCCCCCTCGCTGCTGCTGCCCCCTCTGCCCCCTCGCTCGTC	733
OY		605	GGGACTCTCTGCGCGCGCGCTGAGCCCTCCGCGGACTCTTGTGTAACTGAGCCCTCTGC	664
Dd		732	CCTCTCTGCTCTGCGCCCCCTCGCTGTGCCCCCTCTCTCTCTCTCTGCCCCCTCTGCCCCCTTC	673
OY		665	GAGCGCTCATCTGAGTGTGCTTTGAGAGCGCCTTCTGAGCGGCGCTGAGTGCACCCACAGCT	724
Dd		672	TGCCCTCTCTCTGCTGCTCTGCCCCCTTCCTGCTCTGCTCTGCCCCCTCTGCCCCCTCTG	613
OY		725	TCCGGGAGGCGCTGTGCGCGGCTGTGAGACTACACCGCAGACCACTATTATCATCATCTTGC	784
Dd		612	TGCTCTGCCCCCTCTCTCCGCTCTGCCCCCTCTGCCCCCTCTGCCCCCTCTGCTGCTG	553
OY		785	AAGGCGACAGAGGGCGACCCCCCGGACACCGGCGCTCTGCTGTGGCGACAGCAGCGCACG	844
Dd		552	TGCCCTCTCTGCGCCCCCTCGCTGTGCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	493
OY		845	TGCTGACCTTGTCTGCTGTGAGAGGCC	870
Dd		492	TCTGCCCCCTCTCTCTGCTCTGCCCC	467
		RESULT 14		
		ID AAA75454/C		
		AAA75454 standard; DNA; 2580 BP.		
XX		AAA75454;		
AC				
XX		15-JAN-2001 (first entry)		
DT				
DE		Nucleotide sequence of the Epstein Barr nuclear antigen.		
XX				
KW		Origin of replication; protein-protein interaction; replication; two-hybrid system; nuclear antigen; ss.		
OS		Epstein-Barr virus.		
PN		US611411-A.		
PD		05-SEP-2000.		
PF		30-MAR-1998; 98US-0050863.		
PR		30-MAR-1998; 98US-0050863.		
PA		(RIGE-) RIGEL PHARM INC.		
PI		Luo Y, Payan D, Huang B;		
DR		WPT; 2000-593546/56.		
XX				

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 18:26:01 : Search time 62 Seconds
(without alignments)
734.520 Million cell updates/sec

Title: US-09-598-443-2
Perfect score: 2147
Sequence: 1 MPGVCDRAPFLSPEDQVL.....GSRNYSARTDFYCLVSKDM 410

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequid: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_032802:*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2147	100.0	410	20	AAV25426
2	2147	100.0	410	22	AAAB61139
3	1761	82.0	407	22	AAU17408
4	1761	82.0	407	22	AAAM3652
5	1761	82.0	410	22	AAAM3583
6	1749	81.5	363	21	AAAB58416
7	974.5	45.4	212	22	AAAM5854
8	267.5	12.5	658	20	AAV22164
9	267.5	12.5	686	20	AAV14128
10	257.5	12.0	579	20	AAV14130
11	256.5	11.9	481	22	ABBI0347

12	256.5	11.9	486	20	AAV14129	Human IL-1R10 pro
13	256.5	11.9	696	21	AAV95298	Human Xrec2. Homo
14	256.5	11.9	696	22	AAW78808	Human protein SEQ
15	256.5	11.9	710	22	ABBI1785	Human oligophrenin
16	256.5	11.9	710	22	AAW79792	Human protein SEQ
17	254	11.8	519	19	AAW77140	Murine interleukin
18	254	11.8	519	20	AAV39781	Interleukin-18 rec
19	254	11.8	537	18	AAW31908	Mouse receptor pro
20	254	11.8	537	20	AAV06615	Mouse interleukin-
21	232	10.8	521	20	AAV39780	Interleukin-18 rec
22	232	10.8	540	19	AAW77145	Human interleukin-
23	232	10.8	540	20	AAV39786	Interleukin-18 rec
24	231.5	10.8	541	18	AAW31907	Human receptor pro
25	231.5	10.8	541	20	AAV06613	Human interleukin-
26	229.5	10.7	570	17	AAW01911	Human interleukin-
27	215.5	10.0	570	17	AAW01913	Mouse interleukin-
28	209.5	9.8	553	14	AAW2060	IL-1R. Homo sapie
29	209.5	9.8	569	10	AAW92001	Derived sequence o
30	209.5	9.8	569	10	AAW90330	Human interleukin-
31	209.5	9.8	569	15	AAW59090	Human interleukin-
32	209.5	9.8	569	15	AAW60870	Human IL-1 recepto
33	209.5	9.8	569	17	AAW30376	Human interleukin-
34	209.5	9.8	569	18	AAW22733	Human interleukin-
35	209.5	9.8	569	18	AAW06541	Human interleukin-
36	209.5	9.8	569	21	AAW37791	Human interleukin-
37	209.5	9.8	569	22	AAW30921	A human interleukin
38	209.5	9.8	569	22	AAW59700	Human interleukin-
39	204.5	9.5	561	17	AAW91065	Rat interleukin-1
40	204.5	9.5	561	22	AAE06665	Rat interleukin-1
41	204.5	9.5	561	22	AAE03539	Rat interleukin-1
42	204	9.5	562	17	AAW31064	Human interleukin-
43	204	9.5	562	22	AAE06664	Human interleukin-
44	204	9.5	562	22	AAE03538	Human interleukin-
45	202	9.4	556	22	AAE00275	Transmembrane form

ALIGNMENTS

RESULT 1	
AAV25426	AAV25426 standard; Protein: 410 AA.
XX	AC AAV25426;
XX	DT 08-SEP-1999 (first entry)
XX	DE Human SIGIRR protein.
XX	KW SIGIRR: anti-inflammatory; anti-autoimmune disease; chromosome 11;
KW	interleukin-1 receptor; IL15.5; arthrogryposis multiplex congenita;
KW	breast cancer; insulin-dependent diabetes; sickle cell anaemia;
KW	bladder cancer; detection; cell-signal transduction; gene therapy;
KW	immune regulation; cell proliferation; cell death; cell migration;
KW	cell interaction; inflammation; marker; mass spectrometry; human.
XX	
OS	Homo sapiens.
XX	
PN	W09932626-A1.
XX	
PD	01-JUL-1999.
XX	
PE	23-DEC-1998; 98WO-US27368.
XX	
PR	23-DEC-1997; 97US-0068770.
XX	
PA	(IMMUNEX CORP.
XX	
PI	Sims JE;
XX	
DR	WPI: 1999-418925/35.
DR	N-PSDB: AAX88091.
XX	

PT New interleukin-1 receptor analog SIGIRR nucleic acid and proteins
XX
PS Claim 2; Page 69-71; 72pp; English.

CC This invention describes a novel human SIGIRR DNA, its allelic variants
CC or species homologues which have anti-inflammatory and anti-autoimmune
CC disease activity. SIGIRR is an analog of interleukin-1 receptor. The
CC products of the invention are used (a) as probes or primers for
CC identifying human chromosome 11, to map genes on this chromosome and to
CC identify disease-related genes (particularly in the region 11p15.5 where
CC genes are present associated with e.g. arthrogryposis multiplex
CC congenita, breast cancer, insulin-dependent diabetes, sickle cell
CC anaemia, bladder cancer), including detection of defective genes; (c)
CC to study cell-signal transduction and the SIGIRR system, and (d) in
CC gene therapy. Sense and antisense oligonucleotides can be used to inhibit
CC expression of the SIGIRR gene. The proteins of the invention are used:
CC (i) to study cellular processes (immune regulation, proliferation, death,
CC migration, interaction with other cells and inflammation); (ii) to
CC identify and purify proteins that associate with SIGIRR ligands and
CC receptors, and to measure their biological activity; (iii) in screening
CC for, and rational design of potential inhibitors of activity; (iv)
CC therapeutically against diseases mediated by SIGIRR polypeptide
CC counter structures; (v) as molecular weight (m.w.) markers in
CC electrophoresis; (vi) for determining isoelectric points of unknown
CC proteins; (vii) as controls for determining the extent of protein
CC fragmentation (e.g. to aid characterization of protein structures by
CC mass spectrometry); (viii) for generation of antibodies (Ab); (ix) to
CC deliver diagnostic or therapeutic agents to cells that express SIGIRR
CC binding molecules.

XX
SQ Sequence 410 AA:

Query Match 100.0%; Score 2147; DB 20; Length 410;
Best Local Similarity 100.0%; Pred. No. 7.6e-220;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGVCDRAPDFLSPEDQVLRPALGSSVALNCTAMVYSGPHCSLPYQWKDGLPLGIGG 60
DB 1 MPGVCDRAPDFLSPEDQVLRPALGSSVALNCTAMVYSGPHCSLPYQWKDGLPLGIGG 60
QY 61 HYSLHEYSWKANLSEVLVSSVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHYA 120
DB 61 HYSLHEYSWKANLSEVLVSSVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHYA 120
QY 121 AVLASLVLALLLAAALLYVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSDCPEDRKF 180
DB 121 AVLASLVLALLLAAALLYVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSDCPEDRKF 180
QY 181 VNFILKPOLERRRGYKFLDQDRLPRAEPSADLLVNLSRCRRLIYVLSDAFLSRAMCSH 240
DB 181 VNFILKPOLERRRGYKFLDQDRLPRAEPSADLLVNLSRCRRLIYVLSDAFLSRAMCSH 240
QY 241 SFREGLCRLLELTPRPLFTIFEGORDPAHPALRLLRHRLVTLMLRPGSVTPSSDFW 300
DB 241 SFREGLCRLLELTPRPLFTIFEGORDPAHPALRLLRHRLVTLMLRPGSVTPSSDFW 300
QY 301 KEVQOLAPRKVRYPVEGDPQDLODDKDPMLILGRVREGALDSEVDPDEGLGVRG 360
DB 301 KEVQOLAPRKVRYPVEGDPQDLODDKDPMLILGRVREGALDSEVDPDEGLGVRG 360
QY 361 PVGGEPAHPHTSGVSLGESRSSEVDVSDLSRNTSARTDFCYLXKDDM 410
DB 361 PVGGEPAHPHTSGVSLGESRSSEVDVSDLSRNTSARTDFCYLXKDDM 410

RESULT 2
ID AAB61139 standard; Protein; 410 AA.
XX AAB61139;
AC AAB61139;
XX
DT 30-MAR-2001 (first entry)

XX Human NOV9 protein.
DE
XX
KM Human; NOVX; antiinflammatory; cytosstatic; neuroprotective;
KM cerebrioprotective; immunomodulator; vunerary; vasotrophic; gene therapy;
KM hyperplasia; tumour; restenosis; psoriasis; Dupuytren's contracture;
KM diabetes; Rheumatoid arthritis; cerebral oedema; Alzheimer's disease.
XX
OS Homo sapiens.
PN WO200075321-A2.
PD 14-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15303.
XX
PR 03-JUN-1999; 99US-0137322.
PR 16-MAR-2000; 2000US-0189810.
PR 22-MAR-2000; 2000US-0191158.
PR 30-MAR-2000; 2000US-0193086.
PR 31-MAY-2000; 2000US-0137322.
XX
PA (CURA-) CUBAGEN CORP.
XX
PI Shinkets RA, Fernandes E, Herrman J, Vernet C;
XX
XX WPI: 2001-102403/11.
DR N-PSDB; AAF27857.
XX
PT New NOVX polypeptides and polynucleotides, useful in gene therapy, as a
PT diagnostic marker, protein therapeutic, antibody or small molecule drug
PT target for treating immune, proliferative and metabolic diseases and
PT wound healing -
XX
PS Claim 1; Page 36-38; 194pp; English.

CC The present sequence is a new isolated polypeptide (NOVX). The NOVX
CC polypeptides, NOVX nucleic acids, and anti-NOVX antibodies are useful for
CC treating or preventing NOVX-associated disorders. They are also useful
CC for determining the presence of or a predisposition to a disease
CC associated with altered levels of the NOVX polypeptide or nucleic acid.
CC These NOVX-associated disorders include hyperplasias, tumours,
CC restenosis, psoriasis, Dupuytren's contracture, diabetic complications,
CC rheumatoid arthritis, cerebral lesions, diabetic neuropathies, cerebral
CC oedema, senile dementia or Alzheimer's disease. The NOVX polynucleotides
CC are especially useful in gene therapy. Specifically, NOVX is useful as
CC a diagnostic marker or prognostic marker, protein therapeutic and
CC antibody target or small molecule drug target to treat disorders in the
CC immune response pathway, thyroid and metabolic diseases, bone metabolic
CC disorders, diseases of the pancreas (e.g. diabetes or digestive
CC disorders), proliferative diseases, or tissue regeneration and
CC development (e.g. wound healing or treatment of burns).

XX
SQ Sequence 410 AA:
Query Match 100.0%; Score 2147; DB 22; Length 410;
Best Local Similarity 100.0%; Pred. No. 7.6e-220;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGVCDRAPDFLSPEDQVLRPALGSSVALNCTAMVYSGPHCSLPYQWKDGLPLGIGG 60
DB 1 MPGVCDRAPDFLSPEDQVLRPALGSSVALNCTAMVYSGPHCSLPYQWKDGLPLGIGG 60
QY 61 HYSLHEYSWKANLSEVLVSSVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHYA 120
DB 61 HYSLHEYSWKANLSEVLVSSVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHYA 120
QY 121 AVLASLVLALLLAAALLYVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSDCPEDRKF 180
DB 121 AVLASLVLALLLAAALLYVKCRNLVLMYQDAYGEVEINDGKLYDAYVYSDCPEDRKF 180
QY 181 VNFILKPOLERRRGYKFLDQDRLPRAEPSADLLVNLSRCRRLIYVLSDAFLSRAMCSH 240
DB 181 VNFILKPOLERRRGYKFLDQDRLPRAEPSADLLVNLSRCRRLIYVLSDAFLSRAMCSH 240

Db 181 VNFILKPOLERRRGYKFLDLDRLLPRAEPSADLLVNI.SRCRLLIYVLSDAFLSRACSH 240
QY 241 SFRGGLCRLELETRRRPIFTFEGORRPAHPALRLRQHRHLVTLTMRPGSVTPSSDFW 300
Db 241 SFRGGLCRLELETRRRPIFTFEGORRPAHPALRLRQHRHLVTLTMRPGSVTPSSDFW 300
QY 301 KEYVALPRKVRVRRPVGDDPOTQLQDDKDPMLILRGVPRGALDSEVDPPEGDLGVRG 360
Db 301 KEYVALPRKVRVRRPVGDDPOTQLQDDKDPMLILRGVPRGALDSEVDPPEGDLGVRG 360
QY 361 PVGEPSPAPHTSGVSLGESRSSEVDVSLGSRNYSARTDPYCLVSKDM 410
Db 361 PVGEPSPAPHTSGVSLGESRSSEVDVSLGSRNYSARTDPYCLVSKDM 410

RESULT 3
AAU17408
IT AAU17408 standard; Protein; 407 AA.
X AAU17408;
AC AAU17408;
XX
DT 07-NOV-2001 (first entry)
XX
DE Novel signal transduction pathway protein, Seq ID 973.
XX
XX Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;
KM antinflammatory; anti-HIV; antibacterial; antinflammatory; cancer;
KM immune system disorder; rheumatoid arthritis; inflammatory condition;
KM organ transplant rejection; infection; hepatitis C; blood disorder;
KM sickle cell anemia; hyperproliferative disorder; Gaucher's disease;
KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KM chromosomal abnormality; Down syndrome; ischemia; renal disorder;
KM cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KM reproductive system; gastrointestinal; liver disorder; AIDS;
KM acquired immune deficiency syndrome.
XX
XX Homo sapiens.
OS
PN MO200154733-A1.
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01312.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
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 PR 01-SEP-2000; 2000US-0229343.
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 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
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 PR 25-SEP-2000; 2000US-0234997.
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 PR 08-NOV-2000; 2000US-0246477.

PR 08-NOV-2000; 2000US-0246478.
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 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
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 PR 17-NOV-2000; 2000US-0249210.
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 PR 17-NOV-2000; 2000US-0249213.
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 PR 05-DEC-2000; 2000US-0251988.
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 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251899.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM.
 PI WPI; 2001-488781/53.
 DR N-PSDB; AAI63958.
 DR
 XX
 PT
 PT
 XX
 PS
 XX
 CC Claim 11; SEQ ID NO 330; 664bp + Sequence Listing; English.
 CC
 CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
 CC the encoded proteins (AAW434497-AAW43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC colitis; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the

XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX
XX
XX Claim 11: Page 1271-1272; 1425pb; English.
XX
XX Polynucleotide sequences AAF17962 - AAF18424 encode human lung cancer
CC associated proteins represented in AAS58106 - AAS85548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardiactive; and
CC immunomodulatory; muscular active general; vulnerrary; gastrointestinal
CC general; nephrotoxic; antifibrotic; gynecological; or antibacterial
CC activity. The invention also includes antithodias specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromsome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive, and
CC gastrointestinal, plimonal, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAS8549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX
XX Sequence 363 AA;

Query Match	81.58;	Score 1749;	DB 21;	Length 363;
Best Local Similarity	99.48;	Pred. No. 1.7e-177;		
Matches 339;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	70	VKANLSEVYVSSVLQVNTSTREYVGAFTCSIONSSSFILORAGTSTHVAVLASLLVL	129
Db	23	VKANLSEVYVSVLQVNTSTREYVGAFTCSIONSSSFILORAGTSTHVAVLASLLVL	82
QY	130	LALLLAALYYVCRNLVTLVMTQDAVGEYINDCIKLDAVYSDCPEBKRPFNFIKPOL	189
Db	83	LALLLAALYYVCRNLVTLVMTQDAVGEYINDCIKLDAVYSDCPEBKRPFNFIKPOL	142
QY	190	ERRRGKFLDLDRDILLPAPEPSADLVNLSRCRLIYVLSDFLSPAMSHSFRGICRL	249
Db	143	ERRRGKFLDLDRDILLPAPEPSADLVNLSRCRLIYVLSDFLSPAMSHSFRGICRL	202
QY	250	LELTRRPIITTEGGRORPAPARLRLRORRHVYTLILMRPSYVSSPFKEVOLALPR	309
Db	203	LELTRRPIITTEGGRORPAPARLRLRORRHVYTLILMRPSYVSSPFKEVOLALPR	262
QY	310	KAVYRVEEDPOTOLQDDKDKMLILKRVRVEGRALDSEVDPPDEGLVYRGVYGEPSAP	366
Db	263	KAVYRVEEDPOTOLQDDKDKMLILKRVRVEGRALDSEVDPPDEGLVYRGVYGEPSAP	322
QY	370	PHHSYGLGESSRSSEVDVSDLGSSNNYSARFDTCVLVSKODM	410
Db	323	PHHSYGLGESSRSSEVDVSDLGSSNNYSARFDTCVLVSKODM	363

RESULT	7
AAM25854	
ID	AAM25854 standard; Protein; 212 AA.
XX	
XX	
AC	AAM25854;
XX	
DT	16-OCT-2001 (first entry)
DE	Human protein sequence SEQ ID NO:1369

KM Human; cancer; HIV infection; human immunodeficiency virus;
KM antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KM antibacterial; endocrine; cardiant; central nervous system; viricide;
KM anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;
KM antipregnant; haemostatic; vulnery; antifur; osteopathic; eczema;
KM dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

XX	neuroproliferative; antidepressant; nootropic; antiparkinsonian; infection;
KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW	antiinflammatory; rheumatoid arthritis; septic shock; pancreatitis;
KW	cardiac dysfunction; neuropathology; cardiac myopathy; autoimmune;
KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW	thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW	allergic rhinitis; diabetes; multiple sclerosis; depression;
KW	Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW	neurological disorder.
XX	
OS	Homo sapiens.
XX	
FN	WC0200153455-A2.
XX	
PD	26-JUL-2001.
XX	
PF	22-DEC-2000; 2000WO-US35017.
XX	
PR	23-DEC-1999; 99US-0471275.
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
XX	
PA	(HYSEQ) HYSEQ INC.
PI	Tang YT, Liu C, Dormanac RT;
XX	
DR	WPI, 2001-457603/49.
XX	
DR	N-PSDB; AAAH9795.
XX	

PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX
Claim 20; Page 282; 1217pp; English.
PS
PS

CC AAH9916 to AAH9904 encode the human proteins given in AAH25225 to
CC AAH25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antinflammatory; antipneumatic;
CC antithrombotic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; vincidine; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antinaemic; antiangiogenic; haemostatic; vulnereary;
CC anticancer; osteoporotic; dermatological; antiallergic; antistaphitic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC infections, autoimmune, genetic diseases, hematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

Query Match	45.48;	Score 974.5;	DB 22;	Length 212;
Best Local Similarity	89.28;	Pred. No. 3e-95;		
Matches 189;	Conservative	0;	Mismatches	0;
			Indels	23;
			Gaps	1

QY	222	RLRIIVLSAPFLSRAMCSHSF-----	-REGGCRLELTETLRPIF	258
Db	1	RLRIIVLSAPFLSRAMCSHSFPGVPGANGVSPAPLTPLTPRRREGCLRLELTETLRPIF		60
QY	259	ITFEQGRRPAPAPARLLRQRRHHVYTLMLRRPESYTPSSDFKAEQVALPKRYVYRVEG		318
Db	61	ITFEQGRRPAPAPARLLRQRRHHVYTLMLRRPESYTPSSDFKAEQVALPKRYVYRVEG		1200
QY	319	DPQTQLQDDKDPMLILKRGVREGALDSEVDPDPBBDLCVGRPVGEPSAPPHITSGVSLG		378
Db	121	DPQTQLQDDKDPMLILKRGVREGALDSEVDPDPBBDLCVGRPVGEPSAPPHITSGVSLG		1800

QY 379 ESRSEVDVSDGSRNYSARTDFYCLVSKDDM 410
|||||
DB 181 ESRSEVDVSDGSRNYSARTDFYCLVSKDDM 212

RESULT 8
AAV22164
ID AAV22164 standard; Protein; 658 AA.
XX
AC AAV22164;

XX 08-SEP-1999 (first entry)
XX
DE Human TIGIR protein sequence.
XX

XX TIGIR; human; chromosome X; FG syndrome; premature ovarian failure-1;
XX leiomyomatosis; epilepsy; Bazex syndrome; detection; defective gene;
XX cell-signal transduction; gene therapy; inhibitor; immune regulation;
XX cell proliferation; inflammation.

XX OS Homo sapiens.

XX PN WO932629-A1.

XX PD 01-JUL-1999.

XX PF 23-DEC-1998; 98WO-US27625.

XX PR 23-DEC-1997; 97US-0068634.

XX PA- (IMMV) IMMUNEX CORP.

XX Sims JE;

XX WPI; 1999-418928/35.

XX DR- N-PSDB; AAX84308.

XX PT New interleukin-1 receptor analog TIGIR nucleic acid and proteins
XX used to, e.g. treat autoimmune disease

XX PS Claim 2; Page 10; 79pp; English.

XX This sequence is the human TIGIR protein of the invention. The
CC TIGIR DNA sequences can be used: (a) as probes or primers for
CC identifying nucleic acid that encodes proteins with TIGIR activity;
CC (b) to identify human chromosome X, to map genes on this chromosome
CC and to identify disease-related genes (particularly in the region
CC Xq21.3-22 where genes are present associated with e.g. FG syndrome,
CC premature ovarian failure-1, leiomyomatosis, epilepsy, Bazex syndrome
CC etc.) including detection of defective genes; (c) to study cell-signal
CC transduction and the TIGIR system, and (d) in gene therapy. Sense and
CC antisense oligonucleotides derived from the TIGIR coding sequence can be
CC used to inhibit expression of the TIGIR gene. The TIGIR protein, or its
CC soluble fragments, are used: (i) to study cellular processes (immune
CC regulation, proliferation, death, migration, interaction with other cells
CC and inflammation); (ii) to identify and purify proteins that associate
CC with TIGIR ligands and receptors, and to measure their biological
CC activity; (iii) in screening for, and rational design of, potential
CC inhibitors of activity; (iv) therapeutically against diseases mediated by
CC TIGIR polypeptide counter-structures; (v) as molecular weight markers in
CC electrophoresis; (vi) for determining isoelectric points of unknown
CC proteins; (vii) as controls for determining the extent of protein
CC fragmentation (e.g. to aid characterisation of protein structures by mass
CC spectrometry); (viii) for generation of antibodies (Ab); and (ix) to
CC deliver diagnostic or therapeutic agents to cells that express TIGIR
CC binding molecules. Ab are used for affinity purification of TIGIR;
CC therapeutically to inhibit binding of TIGIR to its counter structures,
CC and (if agonistic) to promote cell signalling.

XX Sequence 658 AA;

Query Match 12.5%; Score 267.5; DB 20; Length 658;

Best Local Similarity 27.2%; Pred. No. 4, 2e-19;
Matches 103; Conservative 72; Mismatches 143; Indels 60; Gaps 19;

QY 6 DRAPDPLSPSEDO--VLRPALGSSVALNCTAWY-VSGPHOSLPSYQWMLK-DGLPLIGIGH 61
DB 209 DKPPKPLPFMEONPSVIDVOLGKPLNIPCKAFPGFSGE--SGPMIYMWGKFTIEELAGH 266
QY 62 YSLHEYSWKANLSE-----VLSSVLGVNVTSTVEYGAFTCSIONIS--FSSFTLOR 112
DB 267 IRGGEIRLKEHGEKEVEELALIFDSVENDLAN-----YTHVENRNKRKIASVLRK 320
QY 113 AGPTSHV--AAVLASLLVLLALLAALVYKCRNLVNLWQDAYGVEIN-DGKLYDAYV 169
DB 321 KDLIYKIELAGLGALIFLLVLLV--VIYKYNIEFLMFLYRQHFADETNDKREYDAYL 378
QY 170 SYS-----DC--PEDRKRVNFIILKPOLERRRGVYFLDDRLRLRAESADLLVNLK 220
DB 379 SYTKVQDPTLDCNPEEDQALEVLPDVELEKHGYKFLFPERDLPSGYMEDLTRVEDQ 438
QY 221 CRLLIYVLS-DAPLSRAWCSHSFREGICRL--ELTRRPIFTFEGORRDPAPALRL 276
DB 439 SRLLIIVLPFDYILTRKGSIFELSLRNHNLVSGEL--KYIILECTELKGVNCOQVESL 496
QY 277 RQHRHLVTLILMRPGSVTP--SSDFKKEVOLALPRVRRPVPVGDPTOLDKDPMLIL 334
DB 497 KRSLKLLSLIKWK-GSKSKLNKGFWKHLVEMPIKKK-----EMLPRCHVLDGAE----- 546
QY 335 RGRVPEGRALDSEVPDP 352
DB 547 -----QGIFGELQIP 557

RESULT 9
AAV14128
ID AAV14128 standard; Protein; 686 AA.
XX
AC AAV14128;
XX
XX 22-JUL-1999 (first entry)
XX
DE Human IL-1RD8 protein sequence.
XX
XX IL-1RD9; IL-1RD8; IL-1RD10; interleukin-1; IL-1receptor DNAX; therapy;
XX IL-1 receptor-like protein; abnormal expression; immunological disorder;
XX inflammatory disorder; morphological disorder.
XX OS Homo sapiens.
XX
XX WO919480-A2.
XX
XX 22-APR-1999.
XX
XX 14-OCT-1998; 98WO-US20939.
XX
XX 10-AUG-1998; 98US-0095987.
XX 15-OCT-1997; 97US-0951829.
XX 17-NOV-1997; 97US-0971635.
XX 12-MAR-1998; 98US-0078008.
XX 18-MAR-1998; 98US-0040714.
XX 15-APR-1998; 98US-0081883.
XX
XX (SCHE) SCHERING CORP.
XX
XX Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;
XX WPI; 1999-326545/27.
XX DR N-PSDB; AAX58245.
XX
XX Interleukin-1 receptor-like polypeptides RD8, 9 and 10
XX
XX Claim 18; Page 93-96; 150pp; English.
XX
XX This sequence is a interleukin-1 (IL-1) receptor-like polypeptide,

CC designated IL-1 receptor DNAx designation 8 (IL-1RD8), of the
 CC invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments
 CC and mutants, also related antibodies, other binding agents and
 CC (ant)agonists are used to treat conditions associated with abnormal
 CC expression of the polypeptide or abnormal expression of, or response to,
 CC their ligands, e.g. immunological, inflammatory or morphological
 CC disorders. They may also be used to screen for binding agents (potential
 CC drugs), diagnostic reagents (to detect the proteins or their ligands) and
 CC to isolate related sequences (to detect the proteins or their ligands) and
 CC anti-idiotypic antibodies as carriers for toxins, radionuclides or other
 CC therapeutic agents, and for affinity purification.

Sequence 686 AA:

Query Match 12.5%; Score 267.5; DB 20; Length 686;
 Best Local Similarity 27.2%; Pred. No. 45; 19; 19;

Matches 103; Conservative 72; Mismatches 143; Indels 60; Gaps 19;

QY 6 DRAPFLSPSEDO--VLRPALGSSVALNCTAMV--VSGPHCSIPSVOMLK-DGLPLGIGH 61
 DB 237 DKPPRPLEPMENQPSVIDOLGKPLNIPCKAFGFSGE--SGPMIYMKGEKFIIELAGH 294
 Q 62 YSLHEYSWKANLSE-----VLVSSVLGVNVTSEYGAFTCSIONIS--FSSFTLOR 112
 DB 295 IREGIRLLKEHLGKEVELALIFDSVEADLAN-----YTCHEVNRNGRKNASVLLRK 348
 QY 113 AGPTSHV--AAVLASLVLALLALILYKCRNLVLMYODAYGEVEIN-DGKLYDAYV 169
 DB 349 KDLYKIETLAGGLGALIFLLVLV--VIYKCYNIETLMLEFROHFGADETNDKREYDAYL 406
 QY 170 SYS-----DC--PEDRKFNVTILKPOLERRRGYKFLDRLDLPRAEADLVNLSR 220
 DB 407 SYTKVDDTLDNDNBEQFALEVPDLYEKHYGKFLFIPERDLIPSGTYMEDLTRRYE 466
 QY 221 CRRLIVYS-DAPLSRAMCSHSFREGICRL--ELTRRPITFTEGQRDPAHPLRL 276
 DB 467 SRRLIIVLPDYLIRKMSIFELSRILHNLVSGET--KVILLECTELGKYNCOEVESL 524
 QY 277 ROHRHLVTLMLPRGSGVTP--SSDFKEVQALPRKRVKRPVGGDQTOLODDKPMIL 334
 DB 525 KRSIKILSLIKWK-GSKSSKLNSKFKHLYEPIKPK--EMLPCHVILDSAE----- 574
 QY 335 RGRVPEGRALDSFVDDP 352
 DB 575 -----QGLFGELOIP 585

RESULT 10
 AAY14130
 ID AAY14130 standard; Protein: 579 AA.

AC AAY14130;
 XX AAY14130;
 DT 22-JUL-1999 (first entry)
 XX
 DE Human IL-1RD8 protein sequence.
 XX
 KW IL-1RD9; IL-1RD8; IL-1RD10; Interleukin-1; IL-1receptor DNAx; therapy;
 KW IL-1 receptor-like protein; abnormal expression; immunological disorder;
 KW inflammatory disorder; morphological disorder.
 OS Homo sapiens.
 XX
 XX W0919480-A2.
 XX
 PD 22-APR-1999.
 XX
 XX 14-OCT-1998; 98WO-US20939.
 XX
 PR 10-AUG-1998; 98US-0095987.
 PR 15-OCT-1997; 97US-0951829.
 PR 17-NOV-1997; 97US-0971635.
 PR 12-MAR-1998; 98US-0078008.

PR 18-MAR-1998; 98US-0040714.
 PR 15-APR-1998; 98US-0081883.
 XX
 PA (SCHE) SCHERING CORP.
 PI Bazan JF, Debets JMA, Kastelein RA, Sana TR, Tjams JC;
 DR WPI: 1999-326545/27.
 N-PSDB; AAX58247.
 XX
 PT Interleukin-1 receptor-like polypeptides RD8, 9 and 10
 PS Claim 20; Page 88-91; 150pp; English.

CC This sequence is a interleukin-1 (IL-1) receptor-like polypeptide,
 CC designated IL-1 receptor DNAx designation 8 (IL-1RD8), of the
 CC invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments
 CC and mutants, also related antibodies, other binding agents and
 CC (ant)agonists are used to treat conditions associated with abnormal
 CC expression of the polypeptide or abnormal expression of, or response to,
 CC their ligands, e.g. immunological, inflammatory or morphological
 CC disorders. They may also be used to screen for binding agents (potential
 CC drugs), diagnostic reagents (to detect the proteins or their ligands) and
 CC to isolate related sequences (to detect the proteins or their ligands) and
 CC anti-idiotypic antibodies, as carriers for toxins, radionuclides or other
 CC therapeutic agents, and for affinity purification.

Sequence 579 AA:

Query Match 12.0%; Score 257.5; DB 20; Length 579;
 Best Local Similarity 28.5%; Pred. No. 4e-18;

Matches 96; Conservative 66; Mismatches 130; Indels 45; Gaps 18;

QY 6 DRAPFLSPSEDO--VLRPALGSSVALNCTAMV--VSGPHCSIPSVOMLK-DGLPLGIGH 61
 DB 232 DKPPRPLEPMENQPSVIDOLGKPLNIPCKAFGFSGE--SGPMIYMKGEKFIIELAGH 289
 QY 62 YSLHEYSWKANLSE-----VLVSSVLGVNVTSEYGAFTCSIONIS--FSSFTLOR 112
 DB 290 IREGIRLLKEHLGKEVELALIFDSVEADLAN-----YTCHEVNRNGRKNASVLLRK 343
 QY 113 AGPTSHV--AAVLASLVLALLALILYKCRNLVLMYODAYGEVEIN-DGKLYDAYV 169
 DB 344 KDLYKIETLAGGLGALIFLLVLV--VIYKCYNIETLMLEFROHFGADETNDKREYDAYL 401
 QY 170 SYS-----DC--PEDRKFNVTILKPOLERRRGYKFLDRLDLPRAEADLVNLSR 219
 DB 402 SYTKVDDTLDNDNBEQFALEVPDLYEKHYGKFLFIPERDLIPSGTYMEDLTRRYE 461
 QY 220 CRRLIVYS-DAPLSRAMCSHSFREGICRL--ELTRRPITFTEGQRDPAHPLRL 275
 DB 462 SRRLIIVLPDYLIRKMSIFELSRILHNLVSGET--KVILLECTELGKYNCOEVES 519
 QY 276 ROHRHLVTLMLPRGSGVTP--SSDFKEVQALPRKRVKRPVGGDQTOLODDKPMIL 310
 DB 520 LKRSIKILSLIKWK-GSKSSKLNSKFKHLYEPIK 555

RESULT 11
 ABB10347
 ID ABB10347 standard; Protein: 481 AA.

AC ABB10347;
 XX ABB10347;
 DT 10-JAN-2002 (first entry)
 XX
 DE Human cDNA SEQ ID NO: 655.
 XX
 XX Human; gene therapy; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; inflammation.

OS Homo sapiens.
XX
PN WO200154474-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01349.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
PR 16-MAR-2000; 2000US-189874P.
PR 17-MAR-2000; 2000US-190076P.
PR 18-APR-2000; 2000US-198123P.
PR 19-MAY-2000; 2000US-205515P.
PR 07-JUN-2000; 2000US-209467P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUN-2000; 2000US-215135P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225213P.
PR 14-AUG-2000; 2000US-225214P.
PR 14-AUG-2000; 2000US-225266P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 14-AUG-2000; 2000US-225759P.
PR 18-AUG-2000; 2000US-226279P.
PR 22-AUG-2000; 2000US-226681P.
PR 22-AUG-2000; 2000US-226688P.
PR 22-AUG-2000; 2000US-227182P.
PR 23-AUG-2000; 2000US-227009P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 06-SEP-2000; 2000US-230437P.
PR 06-SEP-2000; 2000US-230438P.
PR 08-SEP-2000; 2000US-231242P.
PR 08-SEP-2000; 2000US-231243P.
PR 08-SEP-2000; 2000US-231244P.
PR 08-SEP-2000; 2000US-231413P.
PR 08-SEP-2000; 2000US-231414P.
PR 08-SEP-2000; 2000US-232080P.
PR 08-SEP-2000; 2000US-232081P.
PR 12-SEP-2000; 2000US-231968P.
PR 14-SEP-2000; 2000US-232397P.
PR 14-SEP-2000; 2000US-232398P.
PR 14-SEP-2000; 2000US-232399P.
PR 14-SEP-2000; 2000US-232400P.
PR 14-SEP-2000; 2000US-232401P.
PR 14-SEP-2000; 2000US-233063P.
PR 14-SEP-2000; 2000US-233064P.
PR 14-SEP-2000; 2000US-233065P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234977P.
PR 25-SEP-2000; 2000US-234998P.
PR 26-SEP-2000; 2000US-235484P.

PR 27-SEP-2000; 2000US-235834P.
PR 27-SEP-2000; 2000US-235836P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 13-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 13-OCT-2000; 2000US-239937P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241221P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241786P.
PR 20-OCT-2000; 2000US-241787P.
PR 20-OCT-2000; 2000US-241808P.
PR 20-OCT-2000; 2000US-241809P.
PR 20-OCT-2000; 2000US-241826P.
PR 01-NOV-2000; 2000US-244617P.
PR 08-NOV-2000; 2000US-246474P.
PR 08-NOV-2000; 2000US-246475P.
PR 08-NOV-2000; 2000US-246476P.
PR 08-NOV-2000; 2000US-246477P.
PR 08-NOV-2000; 2000US-246478P.
PR 08-NOV-2000; 2000US-246523P.
PR 08-NOV-2000; 2000US-246524P.
PR 08-NOV-2000; 2000US-246525P.
PR 08-NOV-2000; 2000US-246526P.
PR 08-NOV-2000; 2000US-246527P.
PR 08-NOV-2000; 2000US-246528P.
PR 08-NOV-2000; 2000US-246532P.
PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
PR 17-NOV-2000; 2000US-249208P.
PR 17-NOV-2000; 2000US-249209P.
PR 17-NOV-2000; 2000US-249210P.
PR 17-NOV-2000; 2000US-249211P.
PR 17-NOV-2000; 2000US-249212P.
PR 17-NOV-2000; 2000US-249213P.
PR 17-NOV-2000; 2000US-249214P.
PR 17-NOV-2000; 2000US-249215P.
PR 17-NOV-2000; 2000US-249216P.
PR 17-NOV-2000; 2000US-249217P.
PR 17-NOV-2000; 2000US-249218P.
PR 17-NOV-2000; 2000US-249244P.
PR 17-NOV-2000; 2000US-249245P.
PR 17-NOV-2000; 2000US-249246P.
PR 17-NOV-2000; 2000US-249265P.
PR 17-NOV-2000; 2000US-249287P.
PR 17-NOV-2000; 2000US-249289P.
PR 17-NOV-2000; 2000US-249300P.
PR 01-DEC-2000; 2000US-250160P.
PR 01-DEC-2000; 2000US-250391P.
PR 05-DEC-2000; 2000US-251030P.
PR 05-DEC-2000; 2000US-251988P.
PR 05-DEC-2000; 2000US-256719P.
PR 06-DEC-2000; 2000US-251479P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR 08-DEC-2000; 2000US-251899P.
PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.
PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-476161/51.
 DR N-PSDB: ABA06569.

PT Isolated nucleic acid molecule encoding an inflammation-associated
 PT polypeptide is used in preventing, treating or ameliorating a medical
 PT condition.

PS Claim 11: SEQ ID NO: 655; 859pp + Sequence Listing; English.

CC The present invention provides human cDNAs, proteins and related genomic
 CC DNAs. These can be used in the treatment of neural, immune system,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal and proliferative disorders and inflammation. The present sequence
 CC is a protein of the invention.

XX Sequence 481 AA:

Query Match 11.9%; Score 256.5; DB 22; Length 481;
 Local Similarity 26.5%; Pred. No. 3.9e-18;
 Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;

QY 6 DRAPFLSPSEDO--VLRPALGSSVALNCTAWVVSQPHCSLPSYQWLKDGILGIGHYS 63

DB 24 DKPFLILYPMESKLTIOETOLDGSANLTCRAFFGYSQDVS-PLIYWMK-----GEKF 74

QY 64 LHEYS-----W-----VKANLSEVLVSSVLGVNVTSTEVGAFCSIONIS---FSSFTL 110

DB 75 IEDLDENRWESDRIKLEHGEDEVSLIYDSVEEGDLGNSCYVENGNGRRHASVLL 134

QY 111 ORAG--PTSHVAVLASLVLALLLALVVKCRNLVLYWQAYGEVEIN-DGKLYDA 167

DB 135 HRRLMYTVELAGGAILLLVCLVT--IKCYKIEIMLFYRNHFGAEELDGDNKDYDA 192

QY 168 YVSYS-----DCPEDRKVFNFILKPOLERRRGYKLFDDDDLLPRAEPSADLVNL 218

DB 193 YLSTYKVPDQWNOETGEERFALFIDMLEKHGYKLFIPDRDLIPTGYIEDVARCV 252

QY 219 SSCRRLIIVLSDAF--LSRAMCSHSFREGICRLLELTR-RPIFTFEGORRPAHPARLL 276

DB 253 DQSKRLIIVMPFNIVYVRGWSIFLELTRRLNMLVGTGEIKVILLICSELGIMNQVEEVAL 312

QY 277 RQHRHLVTLMLR-PGSVTPSSDEFWKEVQALAPKRVRRPV-----EGDPOTOLQ 325

DB 313 KHTIKLTVIKWHGPKCKNLNSKFWKRLQYEMPER-RLEPITHQALDVSEQGFGLQ 370

RESULT 12
 AAY14129 standard; Protein: 486 AA.

XX AAY14129;

XX 22-JUL-1999 (first entry)

XX Human IL-1RD10 protein sequence.

XX IL-1RD9; IL-1RD8; IL-1RD10; interleukin-1; IL-1receptor DNAX; therapy;

XX IL-1 receptor-like protein; abnormal expression; immunological disorder;

XX inflammatory disorder; morphological disorder.

XX Homo sapiens.

XX W09919480-A2.

XX 22-APR-1999.

XX 14-OCT-1998; 98WO-US20939.

XX 10-AUG-1998; 98US-0095987.

XX 15-OCT-1997; 97US-0951829.

PR 17-NOV-1997; 97US-0971635.
 PR 12-MAR-1998; 98US-0078008.
 PR 18-MAR-1998; 98US-0040714.
 PR 15-APR-1998; 98US-0061883.

XX (SCHE) SCHERING CORP.

XX Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;

XX WPI: 1999-325545/27.

XX N-PSDB: AAX58246.

XX Interleukin-1 receptor-like polypeptides RD8, 9 and 10

XX Claim 18: Page 122-124; 150pp; English.

CC This sequence is a interleukin-1 (IL-1) receptor-like polypeptide,
 CC designated IL-1 receptor DNAX designation 10 (IL-1RD10), of the
 CC invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments
 CC and muteins, also related antibodies, other binding agents and
 CC (ant)agonists are used to treat conditions associated with abnormal
 CC expression of the polypeptide or abnormal expression of, or response to,
 CC their ligands, e.g. immunological, inflammatory or morphological
 CC disorders. They may also be used to screen for binding agents (potential
 CC drugs), diagnostic reagents (to detect the proteins or their ligands) and
 CC anti-idiotypic antibodies, as carriers for toxins, radionuclides or other
 CC therapeutic agents, and for affinity purification.

XX Sequence 486 AA:

Query Match 11.9%; Score 256.5; DB 20; Length 486;
 Best Local Similarity 26.5%; Pred. No. 3.9e-18;
 Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;

QY 6 DRAPFLSPSEDO--VLRPALGSSVALNCTAWVVSQPHCSLPSYQWLKDGILGIGHYS 63

DB 29 DKPFLILYPMESKLTIOETOLDGSANLTCRAFFGYSQDVS-PLIYWMK-----GEKF 79

QY 64 LHEYS-----W-----VKANLSEVLVSSVLGVNVTSTEVGAFCSIONIS---FSSFTL 110

DB 80 IEDLDENRWESDRIKLEHGEDEVSLIYDSVEEGDLGNSCYVENGNGRRHASVLL 139

QY 111 ORAG--PTSHVAVLASLVLALLLALVVKCRNLVLYWQAYGEVEIN-DGKLYDA 167

DB 140 HRRLMYTVELAGGAILLLVCLVT--IKCYKIEIMLFYRNHFGAEELDGDNKDYDA 197

QY 168 YVSYS-----DCPEDRKVFNFILKPOLERRRGYKLFDDDDLLPRAEPSADLVNL 218

DB 198 YLSTYKVPDQWNOETGEERFALFIDMLEKHGYKLFIPDRDLIPTGYIEDVARCV 257

QY 219 SSCRRLIIVLSDAF--LSRAMCSHSFREGICRLLELTR-RPIFTFEGORRPAHPARLL 276

DB 258 DQSKRLIIVMPFNIVYVRGWSIFLELTRRLNMLVGTGEIKVILLICSELGIMNQVEEVAL 317

QY 277 RQHRHLVTLMLR-PGSVTPSSDEFWKEVQALAPKRVRRPV-----EGDPOTOLQ 325

DB 318 KHTIKLTVIKWHGPKCKNLNSKFWKRLQYEMPER-RLEPITHQALDVSEQGFGLQ 375

RESULT 13
 AAY95298 standard; Protein: 696 AA.

XX AAY95298;

XX 12-SEP-2000 (first entry)

XX Human Xrec2.

XX Xrec2; interleukin-1 receptor; human; therapy; inflammation; fever.

XX Homo sapiens.

XX MO200036108-A2.
PN
XX 22-JUN-2000.
PD
XX 14-DEC-1999; 99WO-US29549.
XX PF
XX 14-DEC-1998; 98US-0112163.
XX PR 10-NOV-1999; 99US-0164675.
XX (IMMUNEX CORP.
PA
XX Sims JE, Smith DE, Born TL;
PI
XX MPI: 2000-442387/38.
DR N-PSDB; AAA27919.
XX
PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT ID21, ID22, ID23 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus
XX
PS Claim 21; Page 11; 87pp; English.
XX
XX The present sequence is that of human Xrec2, a member of the
CC interleukin-1 (IL-1) receptor family. The sequence was determined
CC by translation of the nucleotide sequence of isolated IL-1 zeta
CC cDNA (see AAA27919). The invention is directed to novel, purified
CC and isolated IL-1 zeta, IL-1 zeta splice variants (see AAA27918-22)
CC polypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22)
CC encoding such polypeptides, processes for production of recombinant
CC forms of such polypeptides, and their uses. The polypeptides can
CC be used to study cellular processes such as immune regulation, cell
CC proliferation, cell death, cell migration, cell-to-cell interaction
CC and inflammatory responses, to identify proteins associated with
CC IL-1 zeta, to screen for potential inhibitors, and to prepare
CC antibodies. In particular, they can be used to activate and/or
CC inhibit the activation of vascular endothelial cells and
CC lymphocytes, induce and/or inhibit the induction of local tissue
CC destruction and fever, inhibit and/or stimulate macrophages and
CC vascular endothelial cells to produce IL-6, induce and/or inhibit
CC the induction of prostaglandins, nitric oxide synthetase, and
CC metalloproteinases, and upregulate and/or inhibit the upregulation of
CC molecules on the surface of vascular endothelial cells.
XX
XX Sequence 696 AA;
SO
Query Match 11.9%; Score 256.5; DB 21; Length 696;
Best Local Similarity 26.5%; Pred. No. 6.9e-18;
Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;

DB 528 KHTIKLTVIRKMGPKCNKLSNFKWRLQYEMPFK-RIEPIITHEQALDVSOGPGELQ 585
RESULT 14
ID AAM78808 standard; Protein; 696 AA.
XX
XX AAM78808;
AC
XX 06-NOV-2001 (first entry)
DT
XX
XX Human protein SEQ ID NO 1470.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukemia;
KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX
XX MO200157190-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 05-FEB-2001; 2001WO-US04098.
PF
XX
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 22-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0683325.
PR 30-NOV-2000; 2000US-0728422.
PR
XX
XX (HYSEQ-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue A, Yang Y, Wejhrman T, Goodrich R;
XX
XX MPI: 2001-476283/51.
DR N-PSDB; AAK51941.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
PT
XX
XX Claim 20; Page 3744-3746; 6221pp; English.
PS
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 696 AA;
SQ
Query Match 11.9%; Score 256.5; DB 22; Length 696;
Best Local Similarity 26.5%; Pred. No. 6.9e-18;
Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;

QY 6 DRAPDFLSPSEQ--VLRPALGSSVALNCTAMVYSGPHCSLPSVOMLKDGLPLGIGHYS 63
DB DKPPLFLYPMESKLTIGTQIGDSANLTCRAFFGSGDVS-PLIYWMK-----GEKF 289

QY 64 LHEYS-----W-----VKANLSEVLVSSVGLVNTSTREVGATGTCSTQINIS---FSSFTL 110
 DB 290 IEDDENRWESDIKILKEHIGDEVEVSIISLVDSEEGDIGNSCYVENGNGRRHRAVLL 349
 QY 111 QRAG--PTSHVAAYLASLIVLLALLAALVYKCRNLVLLMYODAYEVEIN-DGKLYDA 167
 DB 350 HKRELMTVEELAGGALLLLVCLVT--IKCKYKIEIMLFYRNHFGAEELDDNDKDYDA 407
 QY 168 YVSYS-----DCPEDRKVFNFILKPOLERRRGYKFLDRLDLPRAEPSADLLVNL 218
 DB 408 YLSYTKVPDQWNOETGEEERFALEILPDMLEKHYGKFLIPDRDLIPGTGYIEDVAVRCV 467
 QY 219 SSCRRLIVLSDAF--LSRAWCSHSFREGLCRLLELTR-RPIFTFEGORDDPAHPALRL 276
 DB 468 DQSKRLIIVMTFNVYVRGWSIFELFETRLRNMLVTGEEKVILIECSBELRGIMNYQVEAL 527
 QY 277 ROHRRLVTLMLR--PGSVTPSSDEKWEVOLAPRKVRYPY-----EGDPQTOLO 325
 DB 528 KHTIKLIVYIKWHGPKCNKLNKSKFMKRLQYEMPRK-RIEPTHRQALDVSEOGPFGELO 585

RI 15
 AB 185
 ID ABB11785 standard; peptide: 710 AA.
 AC ABB11785;
 DI 11-JAN-2002 (first entry)

Human oligophrenin-4 homologue, SEQ ID NO:2155.

Human: cytokine; cell proliferation; cell differentiation; growth factor;
 haematopoiesis regulation; tissue growth; immunomodulator; activin;
 inhibin; chemotaxis; chemokinesis; cancer; tumour; haematopoietic disorder;
 myeloid cell disorder; lymphoid cell disorder; ataxia; arthritis;
 chronic inflammatory condition; proliferative retinopathy;
 atherosclerosis; coronary heart disease; arterial ischaemia;
 bone disorder; osteoporosis; vascular growth disorder;
 tissue regeneration; wound healing; infection; immune disorder;
 cell culture; drug screening; gene therapy; antiinflammatory;
 antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
 cytosolic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 antifungal; vulnery; antitumor.

Homo sapiens.

WO200157188-A2.

9-AUG-2001.

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914.

27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI: 2001-457740/49.

N-PSDB: ABA09029.

Human proteins and DNA encoding sequences useful for preventing,
 treating or ameliorating a medical condition in a mammalian subject
 e.g. arthritis and cancer -

Claim 20; Page 248; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

Sequence 710 AA;

Query Match 11.9%; Score 256.5; DB 22; Length 710;

Best Local Similarity 26.5%; Pred. No. 7, 1e-18;

Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;

QY 6 DRAPFLSPSDO--VLRPALGSSVALNCRAMVYSGHCLSPVOMLKQDPLGICGHHS 63
 DB 253 DKPRKLLVPMESKLIQTQIGDSANLTCRAFEGSSDVS-PLIYMKK-----GKRF 303
 QY 64 LHEYS-----W-----VKANLSEVLVSSVGLVNTSTREVGATGTCSTQINIS---FSSFTL 110
 DB 304 IEDDENRWESDIKILKEHIGDEVEVSIISLVDSEEGDIGNSCYVENGNGRRHRAVLL 363
 QY 111 QRAG--PTSHVAAYLASLIVLLALLAALVYKCRNLVLLMYODAYEVEIN-DGKLYDA 167
 DB 364 HKRELMTVEELAGGALLLLVCLVT--IKCKYKIEIMLFYRNHFGAEELDDNDKDYDA 421
 QY 168 YVSYS-----DCPEDRKVFNFILKPOLERRRGYKFLDRLDLPRAEPSADLLVNL 218
 DB 422 YLSYTKVPDQWNOETGEEERFALEILPDMLEKHYGKFLIPDRDLIPGTGYIEDVAVRCV 481
 QY 219 SSCRRLIVLSDAF--LSRAWCSHSFREGLCRLLELTR-RPIFTFEGORDDPAHPALRL 276
 DB 482 DQSKRLIIVMTFNVYVRGWSIFELFETRLRNMLVTGEEKVILIECSBELRGIMNYQVEAL 541
 QY 277 ROHRRLVTLMLR--PGSVTPSSDEKWEVOLAPRKVRYPY-----EGDPQTOLO 325
 DB 542 KHTIKLIVYIKWHGPKCNKLNKSKFMKRLQYEMPRK-RIEPTHRQALDVSEOGPFGELO 599

Search completed: November 7, 2002, 18:49:32
 Job time : 66 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2002, 18:42:16 ; Search time 70 Seconds
(without alignments)
1013.256 Million cell updates/sec

Title: US-09-598-443-2

Perfect score: 2147

Sequence: 1 MPGVCDRAPELSPSEDOVL.....GSRNYSARTDFYCLVSKDDM 410

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequenced: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mmc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_todent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2147	100.0	410	Q9H733	Q9H733 homo sapien
2	1546.5	72.0	409	Q9JL28	Q9JL28 mus musculu
3	267.5	12.5	658	Q9NZNO	Q9NZNO homo sapien
4	267.5	12.5	686	Q9NP60	Q9NP60 homo sapien
5	261	12.2	686	Q9ERS6	Q9ERS6 mus musculu
6	256.5	11.9	696	Q9UJ53	Q9UJ53 homo sapien
7	256.5	11.9	696	Q9UJ53	Q9UJ53 homo sapien
8	254	11.8	537	Q61098	Q61098 mus musculu
9	231.5	10.8	541	Q13478	Q13478 homo sapien
10	228.5	10.6	570	Q14915	Q14915 homo sapien
11	217	10.1	574	Q14915	Q14915 homo sapien
12	215.5	10.0	570	Q61730	Q61730 mus musculu
13	211	9.8	533	Q9DEE1	Q9DEE1 galus galli
14	210.5	9.8	570	Q63621	Q63621 ratius norv
15	210	9.8	533	Q9DEE5	Q9DEE5 galus galli
16	206.5	9.6	575	Q9HB29	Q9HB29 homo sapien

17	204.5	9.5	561	11	Q62929	Q62929 ratius norv
18	204	9.5	562	4	Q13525	Q13525 homo sapien
19	203.5	9.5	573	6	Q9TV71	Q9TV71 equus cabal
20	202	9.4	556	4	Q9UQ44	Q9UQ44 homo sapien
21	196.5	9.2	1346	5	Q9V477	Q9V477 drosophila
22	189.5	8.8	567	11	Q05208	Q05208 mus musculu
23	189	8.8	599	4	Q95256	Q95256 homo sapien
24	184	8.6	555	13	Q90874	Q90874 galus galli
25	183	8.5	566	11	Q62611	Q62611 ratius norv
26	177.5	8.3	614	11	Q92281	Q92281 mus musculu
27	161	7.5	1100	5	Q24622	Q24622 drosophila
28	152.5	7.1	795	5	Q9VJX9	Q9VJX9 drosophila
29	152.5	7.1	795	5	Q9NBK8	Q9NBK8 drosophila
30	150.5	7.0	743	5	Q95RV9	Q95RV9 drosophila
31	150.5	7.0	795	5	Q9XZF9	Q9XZF9 drosophila
32	150.5	7.0	1514	5	Q9VUN0	Q9VUN0 drosophila
33	150.5	7.0	1514	5	Q9NBK9	Q9NBK9 drosophila
34	149.5	7.0	557	5	Q961H0	Q961H0 drosophila
35	149.5	7.0	1385	5	Q9V825	Q9V825 drosophila
36	145.5	6.8	486	13	Q9DEE2	Q9DEE2 galus galli
37	144.5	6.7	486	13	Q9DEE4	Q9DEE4 galus galli
38	144	6.7	784	11	Q9QDN7	Q9QDN7 mus musculu
39	144	6.7	784	11	Q9DBC4	Q9DBC4 mus musculu
40	142.5	6.6	826	6	Q9TSP2	Q9TSP2 papio anub1
41	139.5	6.5	1389	5	Q24591	Q24591 drosophila
42	138	6.4	752	4	Q9UK78	Q9UK78 homo sapien
43	138	6.4	799	4	Q9UM57	Q9UM57 homo sapien
44	138	6.4	839	4	Q00206	Q00206 homo sapien
45	137.5	6.4	1446	5	Q9V820	Q9V820 drosophila

ALIGNMENTS

RESULT 1	Q9H733	PRELIMINARY:	PRT:	410 AA.
ID	Q9H733			
AC	Q9H733			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	CDNA: FLJ21446 FIS, CLONE COL04458.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=COLON;			
RA	Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitaani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,			
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.;			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AK025099; BAB15066.1; -			
DR	InterPro: IPR003600; Ig_Like.			
DR	InterPro: IPR00157; TIR.			
DR	PIfam: PF01582; TIR: 1.			
DR	SMART: SM00410; IG_Like: 1.			
DR	SMART: SM00255; TIR: 1.			
SQ	SEQUENCE 410 AA; 45707 MW; 2A7A663D79567ED6 CRC64;			
Query Match	100.0%; Score 2147; DB 4; Length 410;			
Best Local Similarity	100.0%; Pred. No. 2.8e-197;			
Matches 410; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 MPVCDRAPELSPSEDOVLPAALGSSVALNCAWVSGPHCSLPVOMLKDLPLGIGG 60			
DB	1 MPVCDRAPELSPSEDOVLPAALGSSVALNCAWVSGPHCSLPVOMLKDLPLGIGG 60			
OY	61 HVSLSHEYSWVKANLSEVLVSVLVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHVA 120			
DB	61 HVSLSHEYSWVKANLSEVLVSVLVGVNTSTEVYGAFTCSIONISFSSFTLQRAGPTSHVA 120			

Qy	121	AVISLTLVLTALLLAALYYVACRLNVLTMQADAYGEVEINDDKIXDAVAYSDCEPERKF	180
Db	121	AVLASLTLVLTALLLAALYYVACRLNVLTMQADAYGEVEINDDKIXDAVAYSDCEPERKF	180
Qy	181	VNFILIKPOLERRRGKFLFDRODILPAEBSADLVNISRCRRLTYVLSDFLSRAMCSH	240
Db	181	VNFILIKPOLERRRGKFLFDRODILPAEBSADLVNISRCRRLTYVLSDFLSRAMCSH	240
Qy	241	SFEFGICRLLELTRPRPIITFEQGRDPAIPALFILKORHILVTLIMRGSYTPSSDFW	300
Db	241	SFEFGICRLLELTRPRPIITFEQGRDPAIPALFILKORHILVTLIMRGSYTPSSDFW	300
Qy	301	KEVQALPKVKRYRPEEDPOTQADODKDPMLILKRGVPEGRALDSEVDPPEBGDLVYG	360
Db	301	KEVQALPKVKRYRPEEDPOTQADODKDPMLILKRGVPEGRALDSEVDPPEBGDLVYG	360
Qy	361	PVYGEBSAPPHITSGVSLGESSSEVDYSDLGSRNYSAKTDFTCLVSKDDM	410
Db	361	PVYGEBSAPPHITSGVSLGESSSEVDYSDLGSRNYSAKTDFTCLVSKDDM	410

R#	2
09JLZ8	
ID	09JLZ8
AC	PRELIMINARY:
DT	01-OCT-2000 (TREMBlER, 15)
DT	01-OCT-2000 (TREMBlER, 15) Created
DT	01-DEC-2001 (TREMBlER, 19, last sequence update)
DE	TOLL/INTERLEUKIN-1 RECEPTOR 8.
OS	SIGIRR OR TIRB.
OC	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
FN	[1]
RP	SEQUENCE FROM N.A.
RL	"tirr": a novel toll/interleukin-1 receptor family member.";
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBD databases.
DR	EMBL: AF113795; AAF26200.1; -.
DR	MGI:1344402; Sigirr.
DR	InterPro: IPR003599; IG.
DR	InterPro: IPR003006; IG-MHC.
DR	InterPro: IPR00157; TIR.
DR	Pfam: PF00047; Ig_1.
DR	Pfam: PF01582; TIR; 1.
DR	SMART: SM00409; IG; 1.
DR	SMART: SM00255; TIR; 1.
KY	Receptor.
SEQUENCE	409 AA: 45707 MW; DC4AB99A72356A13 CRC64;

Query Match	72.0%;	Score 1546.5;	DB 11;	Length 409;
Best Local Similarity	72.7%;	Pred. No. 1.1e-139;		
Matches 303;	Conservative 32;	Mismatches 67;	Indels 15;	Gaps 4;

QY	1	MPVCORADDFLSPEDDVLNPRALGSSVALNTCAWVVSOPHCLSPISYOMLKDQGPLTIG	60
QY	1	MAVCVMANPLFSPEDQALFALGREALNTCAWVSPPQCPQSYOMLKDGLALNGS	60
Db	61	HSILHEYSWKNLSEVYVSVLGVNTSTVEYGAFGCSIONISPSFTLQDRAQPTSHA	120
QY	61	HSFLHEDFWVSANFSEI--VSSVLVNLNTNAMEDGTFGCSVMWVSSHSTLRADPAHYA	119
Db	121	AVLASLVLVLLALLAALYYVCGRLVNLWQDYGVEVLNDCKYIDAVYSVSDCEPERKF	180
QY	120	AVLASLVLVLLVALLVYVCRMLNMLLMQDTYREVEYMDCKLDAVYVSDCEPERKF	179
Db	181	VNFIILKPOLERRRKGKFLUDRDLLPAEFSAIDLVLNLSRCRRLTVLVSDFASRAMCSH	240
QY	180	VNFIILKPOLERRRKGKFLFLERDILLPAADASADLVLNLSRCRRLTVLVSDFASRAMCSO	239
QY	241	STPEGSGCRL---LELIRRPILFITFEGORDAPNAPALRL--LRQHRHLYTLMLMRGSV	293

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Db      240  SFREDDCAAYWSSPADLSSAPL-----RARGVSPYTLILSGSRDHRHLYVLLYLMKPGSV 292d
QY      294  TPSSDEPMKEVOALPRKRYRYPREGDPOTQLODDKQPMILILNGRVPREGALDSEVDNPE 353d
Db      293  TPSSDWMKTELQALPRKRYRYPREGDDPQTRLODDKQPMILIVKRAAGSGMSETEIDPPE 352d
QY      354  GDLGVGAPVGFGEPSAPPHITSGVLSGESKSSSEVDYSDLGSRHNSAARTDFCYLASKDDM 410
Db      353  GDLGVGRPAVGFGEPPHITLQETRICTIGESGSMVDYSDLGSRHNSAARTDFCYLASEDDV 409

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RESULT 3		
ID	PRELIMINARY:	PRT: 658 AA.
Q9NZNO		
AC Q9NZNO		
DT 01-OCT-2000 (Tremblrel. 15, Created)		
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN-LIKE 2		

GN ILIRAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20218565; PubMed=10757639;
 RA Jin H., Visswesvariah R., Gardner R.J., Roberts R.G.,
 RT "A novel member of the interleukin-1 receptor gene family, one
 RT deleted in Xp21.3-Xp21.2 mental retardation";
 RL Bae J., Han S., Genest A., Bader J.,
 DR EMBL; AF181285 (AF5412.1); -.
 DR InterPro: IPR003399; Iq.
 DR InterPro: IPR003600; Iq_Like.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR000157; TIR.
 DR Pfam; PF00047; Iq; 3.
 DR Pfam; PF01582; TIR; 1.
 DR SMART; SM00409; Iq; 2.
 DR SMART; SM00410; Iq_Like; 1.
 DR SMART; SM00255; TIR; 1.
 KW Receptor.
 FT
 FQ NON_TER 1 1
 FQ SEQUENCE 658 AA; 75626 MW; 5B7506AF110BB12 CRC64;

Query Match	12.5%;	Score 267.5;	DB 4;	Length 658;
Best Local Similarity	27.2%;	Pred. No. 9.3e-17;		
Matches 103;	Conservative 72;	Mismatches 143;	Indels 60;	Gaps 19

```

QY      6 DRAPDPLSSSEQO--VLPPALGSSVALNCAAW--VSGPHCSIPSYQMLK--GDLPLGIGGH 61
Db      209 DKPPKFLPFEMENQSPVIDVOLGKPLNIPCAAFGFGSGE--SGPMIYMKGKFLFEELAGH 266
QY      62 YSLHEYSWKANLISE-----VLSSVLGNVNSTEYGAFCSSIONIS-----FSSFLQIR 112
Db      267 IREGELRLKEHLGKEVEELALIPDSVVEADLAN-----YCHQENNGKRKHSVYLRR 320
QY      113 AGPTSHV--AAVALSLVLALLLALALYKCLNVLWYQAYGEVEIN--DGLYLAVAY 169
Db      321 KDLIYKIELAGGLGIGLIFLLVLV--VITYCYNIEMLFYRQHFAGADETNDONKEYDAYL 378
QY      170 SYS-----DC--PEDKKFNFNLKPOLERRRGYKLFDDDDLLPRAPEASADLLVLSR 220
Db      379 SYRKVQDDPLDQDNSEEOGFLEVLPRVLEKHGYKLFLEPRDILIPSTYMEDDITRYEQ 438
QY      221 CRLLIIVLS--DAFLSRAMCSHFEGECRL--ELTRRPIPIYEEGGRQRPAPPAIRLL 276
Db      439 SRRLIIVLPDIYLRGMSIFELSRHHNLVSGEI--KVILIECTELKGVNQCEVEST 496
QY      277 RQRHRLVTLTLIRPQSYVP--SSDFWEYQVLAIPKRYVRVPEGQPOLQDDDKDPMLIL 334

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Db 497 KRSTLLSLIWK-GRSKSLNKRKMLHYEMPIKK-----EMLRCHVLDAS----- 546
Qy 335 RGRNPEGRALDSEVDDP 352
Db 547 -----QGLFGELOPIP 557

RESULT 4
Q9NP60 PRELIMINARY; PRT; 686 AA.
Q9NP60:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 15, Last annotation update)
DE ILIRAPL-2 RELATED PROTEIN (INTERLEUKIN-1 RECEPTOR 9) (IL-1 RECEPTOR ACCESSORY PROTEIN-LIKE 2) (TIGIRR-1).
GN ILIRAPL-2 OR ILIR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=ADULT BRAIN;
RA Ferrante M.;
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
RN 2
RP SEQUENCE FROM N.A.
RA Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastalein R.A.;
RT "Computational identification, cloning and characterization of IL-1R9, a novel interleukin-1 receptor (IL-1R)-like gene encoded on human chromosome Xq 22.2-22.3."
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN 3
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Grabowski M., Lorenz B., Hubel R., Strom T.M.;
RT "A gene (ILIRAPL-2) with 61% identity to ILIRAPL maps to Xq22.2."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN 4
RP SEQUENCE FROM N.A.
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S., Slins J.E.;
RT "Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-1R) family. Delineation of a new class of IL-1R-related proteins based on signaling."
RN 5
RA EMBL; AJ290436; CAB89867.1; -
DR EMBL; AF212016; AAF61307.1; -
DR EMBL; AJ272208; CAB86868.1; -
DR EMBL; AF284436; AAC21370.1; -
DR InterPro: IPR003599; IG_
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR004006; IG_MHC.
DR InterPro: IPR004075; Intrikn1_receptor1.
DR InterPro: IPR000157; TIR.
DR Pfam: PF000047; Ig_3.
DR Pfam: PF01583; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00255; TIR; 1.
KW Receptor.
SO SEQUENCE 686 AA; 78669 MW; E400F7ECD186957C CAC64;

Query Match 12.5%; Score 267.5; DB 4; Length 686;
Best Local Similarity 27.2%; Pred. No. 9.9e-17;
Matches 103; Conservative 72; Mismatches 143; Indels 60; Gaps 19;

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QY	62	YSLHYSYVWKNANLSE-----VLVSSYGVGVNTSYEVYGAFCISQIONIS---FSSFTLOR	112
Db	295	IREGEIRILKLEHGLKEVEYELALIFPSVVEADIAN-----YTCHEVNNRGRKHAASVLLRK	348
QY	113	AGPTSHV--AAVVLASLVLLALLLAAALLYVKCRNLVNLMTYODAYEVEIN-DGKLYDAYV	169
Db	349	KDLIYKIELAGLIGLAFILLYLVLLV--VIYKCYNIELMFYRQHFADETNDNKEFYDALV	406
QY	170	SYS-----DC--PEDKKFVNFILKPOLERRRGKFLPDRDLPLPRAEPSADLLVNLNR	220
Db	407	SYTKVDQDTLCCDNEEEOFALEYLPDVLKHYGKFLPIPERDLIPSGTYMEDLTRVEQ	466
QY	221	CRLLIVVLS-DAFISRAVCSHSFREGICRLV---ELTFRPIPIITEGORDRPAHRLRL	276
Db	467	SRRLLIVITPDIYILRGMSIFELERLHNLMLYSGEI--KVILICTELKGVKXNCOEVEST	524
QY	277	ROHRLVTLMLLRPGSVTP--SSDFWKEVOTALPKRVRYRPVGGDPQOTLODDKPMIL	334
Db	525	KRSIKLTLIKWK--GSKSKLNSKRWKHLVEMPIKKK---EMLPCHVILDSAE-----	574
QY	335	RGVPEGRALDSEVDPP	352
Db	575	-----OGLFGEIDP	585
RESULT 5			
ID	Q9ERS6	PRELIMINARY;	PRT, 686 AA.
AC	Q9ERS6;		
DT	01-MAR-2001	(TREMBLrel, 16, Created)	
DT	01-MAR-2001	(TREMBLrel, 16, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)	
DE	TTIGRP-1.		
GN	ILIRAPL2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20459050; PubMed=10882729;		
RA	Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,		
RT	Sims J.E.;		
RT	"Identification and characterization of two members of a novel class		
RT	of the interleukin-1 receptor (IL-1R) family. Delineation of a new		
RT	class of IL-1R-related proteins based on signaling."		
RL	J. Biol. Chem. 275:29946-29954(2000).		
DR	EMBL; AF284437; AAC21371.1; -		
DR	MGI; MGI:1913106; I11rap12.		
DR	InterPro; IPR003599; IG_		
DR	InterPro; IPR003600; IG_like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR00157; TIR.		
DR	Pfam; PF00047; IG; 3.		
DR	Pfam; PF01582; TIR; 1.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00410; IG_like; 2.		
DR	SMART; SM00255; TIR; 1.		
SO	SEQUENCE 686 AA; 78797 MW; 36160D1CDE9B8264 CRC64;		
Query Match 12.2%; Score 261; DB 11; Length 686;			
Best Local Similarity 28.9%; Pred. No. 4.2e-16;			
Matches 98; Conservative 65; Mismatches 126; Indels 50; Gaps 18;			
QY	6	DRAPDPLSPEDQ--VLRRPALGSSVALNCTAMV--VSGPHCSLPSYQWLK-DGLPLIGIGH	61
Db	237	DKPRLPLRPMMENQSVIDVQGLKPLNIPCKAFVFGSGE--SGPMIYMKKGKFFIDELAGH	294
QY	62	YSLHYSYVWKNANLSE-----VLVSSYGVGVNTSYEVYGAFCISQIONIS---FSSFTLOR	112
Db	295	IREGEIRILKLEHGLKEVEYELVTLIFDPSVVEADIAN-----YTCHEVNNRGRKHAASVLLRK	348

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OY 113 AGPSTHV--AAVLASLVLALLALLLVKCRNLVNLWYODAYGEVE-INDGKLYDAYV 169
DB 349 KDLTYIELAGLIGAILFILLILL--VYKCYNIEMLEFYORFGDETDONKNEYDAYL 406
OY 170 SYS-----DC--PEDRKFNFIILKPOLERRRGYKFLDRLDRLPRAEPSADLLVNLNR 220
DB 407 SYTKVDQDTLDCDNTNEEDQFALEILPDLVEKHYGKFLIPERDIL---PSGTYIEDLTR 462
OY 221 C---RRLIVLS-DALSRACWSHSFREGLCRL---ELTRRPFTTFEGORDDPAHPA 272
DB 463 CYESGRLIVLTPPYILIRGWSIFELSRLLHNMVSGEI--KVILIECTELKGVNCOE 520
OY 273 LRLRQHLVTLMLR-PGSVTPSSDFWKEVQALPCK 310
DB 521 VESLKHNIKLLSLIMKGPSSKINSKFWKHLVEMPIK 559

RESULT 6
ID Q90J53 PRELIMINARY; PRT; 696 AA.
AC Q90J53;
DE 01-MAY-2000 (TReMBLrel. 13, Created)
DI 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE OLIGOEPHENIN-4 (TIGIR-2).
GN OPN14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94400548; PubMed=10471494;
RA Carle A., Jun L., Blenvenu T., Vinet M.;
RT "A new member of the IL-1 receptor family highly expressed in
RT hippocampus and involved in X-linked mental retardation.";
RN [2]. Genet. 23:25-31(1999).
RP SEQUENCE FROM N.A.
RX MEDLINE=20459050; PubMed=10882729;
RA Born T., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R family proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
DR EMBL: AJ243874; C985604.1; -.
DR EMBL: AF284435; AC821369.1; -.
DR InterPro: IPR003598; I9-C2.
DR InterPro: IPR003006; I9-C2.
DR InterPro: IPR004075; I9-C2.
DR InterPro: IPR000770; SAND.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00047; I9_2.
DR Pfam: PF01582; TIR.
DR PRINTS: PRO1537; INTRILKINR1F.
DR SMART: SM00408; ITC2.1.
DR SMART: SM00258; SAND.1.
DR SMART: SM00255; TIR.1.
KW Immunoglobulin domain.
SQ SEQUENCE 696 AA; 79968 MW; 987ADB503D73C0A9 CRC64;

Query Match 11.9%; Score 256.5; DB 4; Length 696;
Best Local Similarity 26.5%; Pred. NO. 1.1e-15;
Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;
OY 6 DRAPDLSPSEGO--VLRAALSSVALNCTAMVYSGPHCSLPYQWLKDGILPILIGSHYS 63
DB 239 DKRPKLLYMESKLIQIETQLODSANLTCRAFGSGDVS--PLIYWK-----GEKF 289
OY 64 LHEYS-----W-----VANLSEVYSSVGVNTSTVEGAFPGCSIONIS--FSSFTL 110
DB 290 IEDLDENRWESDRIILKEHGEVYSISLIVDSVEBDLGNISCYVENGRRHNASVLL 349

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OY 111 ORAG--PTSHVAAYLASLVLALLLVKCRNLVNLWYODAYGEVEIN-DGKLYDA 167
DB 350 HKRELMTVELAGGAILLLVCLVT--IYKCYKIEIMLEFYRRHNFAGEELDGANKDYDA 407
OY 168 YVSYS-----DQPEDRKFNFIILKPOLERRRGYKFLDRLDRLPRAEPSADLLVNL 218
DB 408 YLSYTKVDDQNNQETGEERFALEILPDMLEKHYGKFLIPDRDLIPTGTYTEDEVARCV 467
OY 219 SECRRLIVLSDAF--LSRACWSHSFREGLCRLTLTR-RPIFTTFEGORDDPAHPALRL 276
DB 468 DSKRLIVLMPYVYVVRGWSIFELTRLRNMLVTGELIKYLIECSRLGNMYOEVEAL 527
OY 277 RQHLVTLMLR-PGSVTPSSDFWKEVQALPCKVRYRPV-----EGDPOTQLO 325
DB 528 KHTIKLVIVIMHGPKCNKLSKFWKRLQYEMPK-RIEPTHEQALDYSEOGPFGELO 585

RESULT 7
ID Q9NZN1 PRELIMINARY; PRT; 696 AA.
AC Q9NZN1;
DE 01-OCT-2000 (TReMBLrel. 15, Created)
DI 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN-LIKE 1.
GN ILIRL1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20218565; PubMed=10757639;
RA Jin H., Wisesvarahan R., Gardner R.J., Roberts R.G.;
RT "Two novel members of the interleukin-1 receptor gene family, one
RT deleted in Xp21.3-Xp21.3 mental retardation.";
RL Eur. J. Hum. Genet. 8:87-94(2000).
DR EMBL: AF181284; U845941.1; -.
DR InterPro: IPR003598; I9-C2.
DR InterPro: IPR003006; I9-C2.
DR InterPro: IPR004075; I9-C2.
DR InterPro: IPR000770; SAND.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00047; I9_2.
DR Pfam: PF01582; TIR.
DR PRINTS: PRO1537; INTRILKINR1F.
DR SMART: SM00408; ITC2.1.
DR SMART: SM00258; SAND.1.
DR SMART: SM00255; TIR.1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 696 AA; 79979 MW; F2BEC371537F9AA0 CRC64;

Query Match 11.9%; Score 256.5; DB 4; Length 696;
Best Local Similarity 26.5%; Pred. NO. 1.1e-15;
Matches 95; Conservative 64; Mismatches 149; Indels 51; Gaps 15;
OY 6 DRAPDLSPSEGO--VLRAALSSVALNCTAMVYSGPHCSLPYQWLKDGILPILIGSHYS 63
DB 239 DKRPKLLYMESKLIQIETQLODSANLTCRAFGSGDVS--PLIYWK-----GEKF 289
OY 64 LHEYS-----W-----VANLSEVYSSVGVNTSTVEGAFPGCSIONIS--FSSFTL 110
DB 290 IEDLDENRWESDRIILKEHGEVYSISLIVDSVEBDLGNISCYVENGRRHNASVLL 349
OY 111 ORAG--PTSHVAAYLASLVLALLLVKCRNLVNLWYODAYGEVEIN-DGKLYDA 167
DB 350 HKRELMTVELAGGAILLLVCLVT--IYKCYKIEIMLEFYRRHNFAGEELDGANKDYDA 407
OY 168 YVSYS-----DQPEDRKFNFIILKPOLERRRGYKFLDRLDRLPRAEPSADLLVNL 218
DB 408 YLSYTKVDDQNNQETGEERFALEILPDMLEKHYGKFLIPDRDLIPTGTYTEDEVARCV 467

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OY 219 SRCRLIYVLSDAF-LSRAMCSHSFREGJLCRLIELTR-RPIFTTEGQRDRPAHPALRL 276
 DB 468 DOSKRLIYVTPYVVRGMSJFELETRLNMLVTGEIKVILECSELGIMNYQVEVAL 527
 OY 277 RQHRHLYVLLMR-PCSVTPSSDFMKEVQALPRKVRYPV-----EGSPQOLO 325
 DB 528 KATIKLITVAKHGPCKNLKNSKWRLOYEMFK-RIBPTHEQALDVSEQPGFELQ 585

RESULT 8

O61098 PRELIMINARY; PRT: 537 AA.
 AC 061098;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE IL-1RIP PRECURSOR.
 GN IL1RL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96223957; PubMed-8626725;
 RA Parnet P., Garika K.E., Bonnett T.P., Dower S.K., Sims J.E.;
 RT "IL-1RIP is a novel receptor-like molecule similar to the type I
 RT interleukin-1 receptor and its homologues TI/ST2 and IL-1R AcP."
 RL J. Biol. Chem. 271:3967-3970(1996).
 DR EMBL; U43673; AAC52457.1; -.
 DR MGD; MGI:105383; IL1RL1.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR004075; IntrIkn1_receptorI.
 DR InterPro: IPR00157; TIR.
 DR Pfam; PF00047; Ig_3.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR01537; INTRLN1RL1F.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00255; TIR; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 537 AA; 61600 MW; B119FEA03355458 CRC64;

Query Match

Best Local Similarity 11.8%; Score 254; DB 11; Length 537;
 Cons 95; Conservative 62; Mismatches 113; Indels 70; Gaps 18;

OY 9 PDFLSPEDOVLRPALGSSVALNCTA-----WVSGPHCSLPSVQ-----WLK 51
 DB 212 PALGPKCEKV-GVELGKQVNLCSASLNKDLFWYSIRKEDSSDPNVEDKRETTTWS 270
 OY 52 DGLPLIGIGHYSLHEYSWKANLSEVLVSSVLCVNTSTEVYGAFTCSION---ISFSS 108
 DB 271 EG-----KLHASKILRFO-----KITENTLVNLYNCTVANEBAIDTKSP 309
 OY 109 LQOR-----AGPTSHVAVLASLVL--LALLLAALLVYKRLNVLKYOD-AYGEVEIN 162
 DB 310 VLVKKEIPIDPGHVFYGVYVLAASVAVCYILCYITKVDLVLYRRAEDETLTLG 369
 OY 163 KLYDAVVS-SDC-PEDRKVFNFILK--PO-LERRGYKFLDRLDRLPRAEPSADLVN 217
 DB 370 KTYDAVVSILKECPENKEVETLPRVLEKQFGYKLCIFERDVVPGAVVEIHSL 429
 OY 218 LSCRLLIYVLSAFLSRAMCSHSFREGJLCR-LLELTRPIFTTEGQRDRPAH----- 270
 DB 430 IEKSRLLIYVLSOSYLNG-ARRELSGLHEALVERKIKIILIEF-----TPASNTFLP 483
 OY 271 PALRLRHRHLYVLLMRPGSVTPSSDFMKEVQALPRK 310
 DB 484 PSLKLSKSTR-----VLKWRADSPSANSRWMKNLYVIMPAK 519

RESULT 9

O13478 PRELIMINARY; PRT: 541 AA.
 AC 013478;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE IL-1RIP PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96223957; PubMed-8626725;
 RA Parnet P., Garika K.E., Bonnett T.P., Dower S.K., Sims J.E.;
 RT "IL-1RIP is a novel receptor-like molecule similar to the type I
 RT interleukin-1 receptor and its homologues TI/ST2 and IL-1R AcP."
 RL J. Biol. Chem. 271:3967-3970(1996).
 DR EMBL; U43672; AAC50390.1; -.
 DR InterPro: IPR003599; Ig_
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR004075; IntrIkn1_receptorI.
 DR InterPro: IPR00157; TIR.
 DR Pfam; PF00047; Ig_3.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR01537; INTRLN1RL1F.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00255; TIR; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 541 AA; 62304 MW; 7173DB9C7BA71D32 CRC64;

Query Match

Best Local Similarity 10.8%; Score 231.5; DB 4; Length 541;
 Cons 99; Conservative 62; Mismatches 126; Indels 67; Gaps 19;

OY 6 DRA---PDFLSPEDOVLRPALGSSVALNCTA-----WVSGPHCSLPSVQWLKDG 53
 DB 209 DRSNIYVPLLGRKLNIV-AVELGKNVRLNCSALNEDVIYKMGFGENSDPRNIHEKEM 267
 OY 54 LPLIGIGHYSLHEYSWKANLSEVLVSSVLCVNTSTEVYGAFTCSIONISFSSFTL 110
 DB 268 RIMTPEG-----KMHASKVLRITENIGESNLNV-----LYNCTVASTGDTKSFIL 313
 OY 111 QR-----AGPTSHV--AAVLASLVLALLLAALLVYKRLNVLKYODAYGEV-INDK 163
 DB 314 VRKADMAIDPGHVFTRGMIAVLIAVAVCYIVYVDLVLFYRHLTRRDETLTDGK 373
 OY 164 KYDAVVS-SDC-----PEDRKVFNFILKPOLERRGYKFLDRLDRLPRAEPSADLVN 218
 DB 374 TYDAVVSILKECPENKEVETLPRVLEKHFYKLCIFERDVVPGAVVDEIHSLI 433
 OY 219 SRCRLIYVLSAFLSRAMCSHSFREGJLCR-----LLELTRPIFTTEGQRDRP 268
 DB 434 EKSRLLIYVLSKYSMENEVRELSGLHEALVERKIKIILIEPT--PYNDFFELPQ----- 487
 OY 269 AHPALMLRHRHLYVLLMRPG-SVTPSSDFMKEVQALPRKVRYPVGGDPQ 321
 DB 488 ---SLKLSKSHR-----VLKWRADKSLSYNSRFWMKNLYVIMPAKT-VKPGRDEP 533
 RESULT 10
 O14915 PRELIMINARY; PRT: 570 AA.
 AC 014915;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE IL-1 RECEPTOR ACCESSORY PROTEIN (MEMBRANE INTERLEUKIN 1 RECEPTOR
 DE ACCESSORY PROTEIN).
 GN IL1RAP.
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Huang J., Gao X., Li S., Cao Z.;
RN Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
RP [2]
RC TISSUE=BRIN;
RA Saito T., Seki N.;
RN Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
RP [3]
RX MEDLINE=98140136; PubMed=9479509;
RA Dale M., Hammond D.W., Cox A., Nicklin M.J.H.;
RT "The human gene encoding the interleukin-1 receptor accessory protein
RT (IL1RAP) maps to chromosome 3q28 by fluorescence in situ hybridization
RT and radiation hybrid mapping."
RL Genomics 47:325-326(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20261666; PubMed=10799889;
RA Jensen L.E., Muzio M., Mantovani A., Whitehead A.S.;
RT "IL-1 signaling cascade in liver cells and the involvement of a
RT soluble form of the IL-1 receptor accessory protein."
RL J. Immunol. 164:5277-5286(2000).
DR EMBL: AF029213; AAB84059.1; -
DR EMBL: AF006537; BAA32421.1; -
DR EMBL: AF016261; AAC39609.1; -
DR EMBL: AF167342; AAF71689.1; -
DR EMBL: AF167335; AAF71689.1; JOINED.
DR EMBL: AF167336; AAF71689.1; JOINED.
DR EMBL: AF167337; AAF71689.1; JOINED.
DR EMBL: AF167338; AAF71689.1; JOINED.
DR EMBL: AF167339; AAF71689.1; JOINED.
DR EMBL: AF167340; AAF71689.1; JOINED.
DR EMBL: AF167341; AAF71689.1; JOINED.
DR InterPro: IPR003599; 19.
DR InterPro: IPR003006; 19_MHC.
DR InterPro: IPR004075; Interf1_receptor1.
DR Pfam: PF000447; 19_1.
DR Pfam: PF01582; TIR; 2.
DR PRINTS: PR01537; INTRNLIRP.
DR SMART: SM00409; IG_2.
DR SMART: SM00255; TIR; 1.
KW Receptor.
SC SEQUENCE 570 AA; 65418 MW; 5F47F8DDECA98B8A CRC64;
Query Match 10.6%; Score 228.5; DB 4; Length 570;
Best local similarity 27.6%; Pred. No. 4, 1e-13;
Matches 91; Conservative 60; Mismatches 150; Indels 29; Gaps 11;
OY 9 PPFLEPSREOVLRPALGSSVALNCTAWVSGPHCSLPVOWLKG-LPLGIGHYSLHEY 67
DB 243 PVIHSPNDHVVYERKEPEGLIPCTVY-FSLMDSRNEFWMTIDGKRPDDTIDVTINE- 300
OY 68 SWVKANLSVLVSSVIG-NTSTEVYGAFTC---SIQNSFSSFTLRAGPTSHVAVL 123
DB 301 SLSHRTDEFTQTLSTIKKTSYEDLKRSYCHARSAKGEVAKAKKQVAPRIVEL 360
OY 124 A---SLVILMLLALLAYVCRNLVLLMYODAYGEV-INDGLYDAYVYSDDCPEDRK 179
DB 361 AGCFGATVLLVILVIVHYW-LEWVLFYAHFTDETITLDGEYDLYVSARNAEEEE 419
OY 180 FVNFLTKPOLERRRGYKFLDDROLIPRAEPSADLYNLSCRLIYVLSDAFTSRAMCS 239
DB 420 FVLLLRGVLENEPEYKICFIDROSLRPGIYTDITLSFTQSKRLVVLSTNNV----- 473
OY 240 HSFRRGCLRLLETRRPFFITFEG-----QRDPAHAPRLRLRQHRHLVTLILMR-PG 291

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DB 474 ---LOGTOALLLEKAGLENMASRCGNINVIIVQKAVKEFKVELKRAKIVLTVIKMGEK 530
OY 292 SVTPSSDFWKEVOLALPRKVRYPVEDDPQ 321
DB 531 SKYPGGRFWKOLQVAMPVKPSRRSSDEQ 560
RESULT 11
OQERS7 PRELIMINARY; PRT; 574 AA.
AC OQERS7;
DT 01-MAR-2001 (Tremblrel, 16, Created)
DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
DE 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE IL-1RNP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20459050; PubMed=10882729;
RA Bort R.E., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
RA Sling J.L.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R related proteins based on signaling."
RL J Biol Chem 275:29546-29554(2000).
DR EMBL: AF284433; Z7529546-29554(2000).
DR HSSP: P14778; 1IRK.
DR InterPro: IPR003599; 19.
DR InterPro: IPR003598; 19_C2.
DR InterPro: IPR003600; 19_Like.
DR InterPro: IPR003006; 19_MHC.
DR InterPro: IPR000157; TIR.
DR Pfam: PF000447; 19_2.
DR SMART: SM001582; TIR; 1.
DR SMART: SM00409; IG_3.
DR SMART: SM00408; IG_C2_2.
DR SMART: SM00410; IG_Like_1.
DR SMART: SM00255; TIR; 1.
KW Immunoglobulin domain.
SC SEQUENCE 574 AA; 65108 MW; A677A77BBFA50A76 CRC64;
Query Match 10.1%; Score 217; DB 11; Length 574;
Best local similarity 23.3%; Pred. No. 5, 3e-12;
Matches 100; Conservative 62; Mismatches 135; Indels 132; Gaps 20;
OY 13 SPSEDOVLRPALGSSVALNCTAWVSGPHCSLPVOWLKG---DGLPL--- 56
DB 131 SPDVYQILP-IGKSGSLNCHLYFPES--CALDSIKWKYKGCSEIKAKKSPSAGKLLVN 187
OY 57 -----GIGGHYSLEY-----SWVKANLSVLVSSV 82
DB 188 NVAVEDGGSYACARLTHGRFTIRNIAVNTKEVEYGRIPNTIYKNNISIEVPGST 247
OY 83 LGV--NVITSTEVYGAFTC---SIO-----NISS 107
DB 248 LIVNCINTIDTKENTMLRCWRVNNLTVDYKDSKRIQGIETNVSILRQIRYTVNIFLK 307
OY 108 FTLORAGP--TSHV-----AAVLASLVLLALLIAL-LYVSCRNLV 147
DB 308 VMEDDGREFTCAGASAYAILIYVPDPFRAYLLGGLMAFLLVVSLFYNSFKIDM 367
OY 148 LWODAYGVEI--NGKAYLDAYVSYSDCPEDRK-----FVNFLTKPOLERRRGYKFLD 200
DB 368 LWYRSAFHTAQAPDDEKLDAYVLPKYPKPSQGDHVDVTLKILPEVLEKQCGKLFIF 427
OY 201 DRDLLPRAPPSADLYNLSCRLIYVLSDAFTSRAMCSHFRGGLC---RILELTRP1 257
DB 428 GRDEFFGQAVASVIDENTIKCRLMLVFAVPSSSGFLKNLSEQIAYVNVALIOHGKVI 487
OY 258 FTTFEGQRDRPAHP-ALRLRLRQHRHLVTLILMRPGSVTPSSD-----FWKEVOLALPRKV 311

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Db 488 LILELEVKDYSTWPEESIOYIROKHAIO---W-DGDFTEQSOCATKTFMKVRYHMPPR- 542
OY 312 RY---RPVE 317
Db 543 RYPASSPVO 551

RESULT 12

061730 PRELIMINARY; PRT; 570 AA.
AC 061730;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE INTERLEUKIN 1 RECEPTOR ACCESSORY PROTEIN PRECURSOR.
GN IL1RAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=95293970; PubMed=7775431;
RA Greenfeder S.A., Nunes P., Kwee L., Labow M., Chizzonite R.A., Ju G.;
RT "Molecular cloning and characterization of a second subunit of the
RT Interleukin 1 receptor complex."
RL J. Biol. Chem. 270:13757-13765(1995).
DR EMBL: X85999; CAA59991.1; -.
DR MGD: MGI:104975; Il1rap.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR004075; Intriknl_receptor1.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR01537; INTRIKNLRIF.
DR SMART: SM00409; IG; 2.
DR SMART: SM00255; TIR; 1.
DR Signal: Receptor.
KW SIGNAL; Receptor.
FT SIGNAL 1 20 POTENTIAL.
SQ SEQUENCE 570 AA; 65740 MW; 4DAB07E0310AFDC5 CRC64;

Query Match 10.0%; Score 215.5; DB 11; Length 570;

Best Local Similarity 25.6%; Pred. No. 7.3e-12;
Matches 85; Conservative 61; Mismatches 153; Indels 33; Gaps 10;

Q 9 PDFLSPEDQVLRPALGSSVALNCTAM--VVSQPHCSLPVSQWLKDG-LPLGIGGHYSLH 65
Db 243 POLYSPNDRVVYKEKEGEELVIPCXYFSFIMDSH---NEVMWTIDGKKRPDDVTIDITIN 299
OY 66 EYEWVANANLSEVLVSSVGLNVTSTEVYGAFTCSION---ISFSSFTIDORAP---TSH 118
Db 300 ESYVSSTEDETRTQILSTIKKVPEDLRNRYVGHARNTKGEADAKVKQKVIIPRYTVE 359
OY 119 VAAVLASLVLALLAALLLYVCRNLVLLMYODAYGEVE-INDGKLYDAYVSYSDCPED 177
Db 360 LAGGFGATVFLVAVLI--VYHYHWMLEWVLFYRAHFGTDETDIDGKEYDLYVYARVVE 417
OY 178 RKRVNFIILKPOLERRRGYKFLDDRDLLPRAEPSADLLVNLSCRRLLIIVLSDAFLSRW 237
Db 418 EEFFVLLTLRGVLENEFGYKLCIFDRSLPGIYTDLFSLFIQKSRRLIIVLSPNYV--- 473
OY 238 CSHSPFEGCLRIELTRRPIFIIFEG-----QRDPAPRALRLRQNHVLTLLMR- 289
Db 474 ----LQGTQALLLELKAAGLENMASRGINIVLYQYKAVKMDKVKELKRAVTVLTIKMG 528
OY 290 PGSVTPSSDFMKVEVOLALPRKYVRYRVEGDPQ 321
Db 529 EKSKYQGRFRWQLOVAMPYKSPRWSNDKQ 560

RESULT 13

Q9DEEL
ID Q9DEEL PRELIMINARY; PRT; 533 AA.
AC Q9DEEL;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE ST2LV.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RX SEQUENCE FROM N.A.
RA Iwahana H.;
RT "Chicken ST2 gene: genomic structure and its products."
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AB041748; BAB20893.1; -.
DR EMBL: AB041741; BAB20893.1; JOINED.
DR EMBL: AB041742; BAB20893.1; JOINED.
DR EMBL: AB041743; BAB20893.1; JOINED.
DR EMBL: AB041744; BAB20893.1; JOINED.
DR EMBL: AB041746; BAB20893.1; JOINED.
DR EMBL: AB041747; BAB20893.1; JOINED.
DR InterPro: IPR003598; Ig.
DR InterPro: IPR003600; Ig_C2.
DR InterPro: IPR003598; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00047; Ig_2.
DR Pfam: PF01582; TIR; 1.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00410; IGC1; 1.
DR SMART: SM00255; TIR; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 533 AA; 61754 MW; 154CE5915BEICE3 CRC64;

Query Match 9.8%; Score 211; DB 13; Length 533;

Best Local Similarity 23.5%; Pred. No. 1.8e-11;
Matches 76; Conservative 75; Mismatches 142; Indels 30; Gaps 13;

QY 12 LSPSEDOVLRPALGSSVALNCTA--WVSQPHCSLPVSQWLKDG-LPLGIGGHYSL-HEXS 68
Db 211 LFKKDEVDLEVEIGAFLSKQARLGIKKOP---IAVTVDVKMAPEVANEKIKQERS 267
OY 69 WYKANLSEVLVSSVGLV-NVTSTEVYGAFTCSIONISFSSFTL-----ORAGPTSHVA 121
Db 268 YFEGQHGEYGEATLTISNIEHTDLOSFSFCVAMNEMGNRTTIVTLRLKKKSGP--NLIM 325
OY 122 VLASLVLALLAALLLYVCRNLVLLMYODAYGEVEI-NDGKLYDAYSY-----SDCP 175
Db 326 IAGFLVFLMSVAVSVALYQSEFVDIVLYRDLFOAYSVDGKIYAPAYIYPPSHSTEAR 385
OY 176 EDRKFYNFILKPOLERRRGYKFLDDRDLLPRAEPSADLLVNLSCRRLLIIVLSDAFLSR 235
Db 386 FVEYFYQIMPDLEKKGCTLTCTIGRDYTPGEDKANAIKRIKSRRLIITLQOLINC 445
OY 236 AMCSHSPFEGCLR-LIELTRRPIFIIFEGO-RDPAPRALRLRQNHVLTLLMR-PGS 292
Db 446 QELNYOHIALYNALIONDRKIVLLEMEKGSYENLOESLRYIKOQGFVK---WKEQHT 502
OY 293 VTP-----SSDFMKVEVOLALPRKYR 312
Db 503 VHPQSSNKFMKVRYHMPVTLR 525

RESULT 14

063621 PRELIMINARY; PRT; 570 AA.
AC 063621;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN.
 GN IL-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96265355; PubMed=8964912;
 RA Liu C., Chalmers D., Maki R., De Souza E.B.:
 RT "Rat homolog of mouse interleukin-1 receptor accessory protein:
 RT cloning, localization and modulation studies.";
 RL J. Neuroimmunol. 66:41-48(1996).
 DR EMBL: U48592; AAB03502.1; -.
 DR InterPro: IPR003599; IG_1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR004075; Intrikn1_receptorI.
 DR InterPro: IPR00157; TIR.
 DR Pfam: PF00047; IG_3.
 DR P_00047; PF01582; TIR; 1.
 DR P_00047; PF01537; INTRIKN1R1F.
 DR S_00047; SM00409; IG; 2.
 DR SMART: SM00255; TIR; 1.
 KW Receptor.
 SO SEQUENCE 570 AA; 65598 MW; 20C3A5478127AABE CRC64;
 Query Match 9.8%; Score 210.5; DB 11; Length 570;
 Best Local Similarity 25.5%; Pred. No. 2.2e-11;
 Matches 86; Conservative 64; Mismatches 144; Indels 43; Gaps 13;
 OY 9 PDFLPSDDOYLRLPALGSSVALNCTA--VYSGPHCSLPVOMIKDGLPLIGIGHSY 61
 DB 243 PHYSFNDRYVYERKPEGLVLPCKVYFSTIMDSH--NEIWTIDCKKDDVDVITII 299
 OY 62 YSLHYSWKANKLSEVLVSVLG-VNTSTEVYGAFTCSION----ISFSFTLORAGP- 115
 DB 300 ESV-----STDEFTQTOLSTIKKVTPELKRKNYCHARNAGEAEQAKYKOKITPP 354
 OY 116 --TSVAVAVLSLVLALLALVYKCRNLVLMYODAYGEVE-INDKRLDAYSYS 172
 DB 355 RYVLEACGFAGVFLVYVLI--VYHYVLEMYLFTFAHGDIDETLLDGEHDIVSYA 412
 OY 173 DCPEDKRYVNFILKPOLERRRGYKFLDRLDLPRAESADLVNLSRCRLIVYSDAF 232
 DB 413 RNADEEEFVLLTKGVLENEFGYKLCIFDRDSFGIVTDETLISIKSRRLVLSPNY 472
 OY 233 LSRWCSHSFREGLCRLLELTRRPIFTFEG-----QRDPAPALRLRLQHRHLVTL 285
 DB 473 V-----LQGTQALLELAKGLENNASRGINIVILVOYKAVKDLKELKRAKSVLT 523
 OY 286 LLMR-PGSVTPSSSDFWKEVOLALPRKRVYRVEGDPQ 321
 DB 524 IKWGEKSKYPQGRFWKOLQVAMPVKKSPRWSSSDKQ 560

Chicken str2 gene: genomic structure and its products.
 RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AB041738; BAB20773.1; -.
 DR EMBL: AB041738; BAB20773.1; -.
 DR InterPro: IPR003599; IG_1.
 DR InterPro: IPR003598; IG_2.
 DR InterPro: IPR003600; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00047; IG_2.
 DR Pfam: PF01582; TIR; 1.
 DR SMART: SM00409; IG; 3.
 DR SMART: SM00408; IG; 2.
 DR SMART: SM00410; IG_Like; 1.
 DR SMART: SM00255; TIR; 1.
 KW Immunoglobulin domain.
 SO SEQUENCE 533 AA; 61755 MW; AB068E5A763EFCE4 CRC64;
 Query Match 9.8%; Score 210; DB 13; Length 533;
 Best Local Similarity 23.5%; Pred. No. 2.2e-11;
 Matches 76; Conservative 75; Mismatches 142; Indels 30; Gaps 13;
 OY 12 LSPSEDOYLRLPALGSSVALNCTA--VYSGPHCSLPVOMIKDGLPLIGIGHSY 68
 DB 211 LPPKDEDVLEVLGAFAFSIKCOARLGIKKOP---IAVYTDVNMKPAVEADEEKIROEFS 267
 OY 69 WVKANLSEVLVSVLG-VNTSTEVYGAFTCSIONISFSFTL-----ORAGPTSHVA 121
 DB 268 YPEGQHOEYEGATLTISNIERTDLOSSFSCVAMNEMGNTRTIVTLRLKKSGP--NVLM 325
 OY 122 VLASLVLALLALVYKCRNLVLMYODAYGEVE-INDKRLDAYVSY-----SDCP 175
 DB 326 IAGFLVFLMSVAVSVLVQSPFVDVLLYRLDPAVSKDDGKITDVAIVYPRSHSEAT 385
 OY 176 EDKRYVNFILKPOLERRRGYKFLDRLDLPRAESADLVNLSRCRLIVYSDAFSLR 235
 DB 386 FVEYFYQIMPDILNKKCGYLCIGRTYDGEDKANIERIKSRRLIITLQOLINC 445
 OY 236 ANCSHSFREGLCRLLELTRRPIFTFEGQ--RRDPAPALRLRLQHRHLVTL 292
 DB 446 QELNIDQIALNALINDTQVILEMEKMSYENLQESLRYITKQGGYK--WKQCHT 502
 OY 293 VTP---SSDFKEVOLALPRKRV 312
 DB 503 VHPQSSNSKFMKRVYHMPVTLR 525

Search completed: November 7, 2002, 18:51:50
 Job time : 74 secs

RESULT 15
 O9DEES PRELIMINARY; PRT; 533 AA.
 AC O9DEES;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ST2L.
 GN ST2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA 'Iwahana=H.;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 18:41:51 ; Search time 26 Seconds
(without alignments)
610.578 Million cell updates/sec

Title: US-09-598-443-2

Perfect score: 2147

Sequence: 1 MGVCDRAFDLPSEDOVL.....GSRNVSARTDFYCLVSKDDM 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sead: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209.5	9.8	569	IL1R_HUMAN	P14778 homo sapien
2	190.5	8.9	576	IL1R_MOUSE	P13504 mus musculus
3	176	8.2	1097	TOLL_DROME	P08953 drosophila
4	168.5	7.8	576	IL1R_RAT	O02955 rattus norv
5	152	7.1	841	IL1R_BOVIN	O94165 bos taurus
6	144	6.7	841	TUR2_MOUSE	O94un7 bos musculus
7	142.5	6.6	826	TUR4_PAPAN	O94sp2 papio anubi
8	142	6.6	833	TUR4_FELCA	P58727 felis silve
9	138	6.4	839	TUR4_HUMAN	O00206 homo sapien
10	135.5	6.3	784	TUR2_BOVIN	O951a9 bos taurus
11	134	6.2	839	TUR4_PANPA	O94ttn0 pan paniscu
12	131	6.1	781	TUR2_CHICK	O94gb6 gallus gall
13	131	6.1	784	TUR2_MACRA	O95m53 macaca fasc
14	131	6.1	793	TUR2_CHICK	O94d78 gallus gall
15	129	6.0	843	TUR4_HORSE	O94m73 equus cabal
16	125	5.8	784	TUR4_HUMAN	O60603 homo sapien
17	124.5	5.8	808	TUR4_MOUSE	O03142 mus musculus
18	121	5.6	784	TUR2_CRIGR	O941f8 cricetus
19	117	5.4	795	TUR6_MOUSE	O94epw9 mus musculus
20	116	5.4	835	TUR4_RAT	O94x05 rattus norv
21	116	5.4	838	TUR4_CRIGR	O94w82 cricetus
22	115	5.3	296	MY88_MOUSE	P22366 mus musculus
23	114.5	5.3	786	TUR1_HUMAN	O15399 homo sapien
24	114.5	5.1	795	MY88_HUMAN	O99836 homo sapien
25	110.5	5.1	795	TUR1_MOUSE	O94epq1 mus musculus
26	110.5	5.1	835	TUR4_MOUSE	O94uq6 mus musculus
27	109.5	5.1	796	TUR6_HUMAN	O942c9 homo sapien
28	107.5	5.0	1032	TUR9_HUMAN	O94r96 homo sapien
29	106.5	5.0	859	TUR5_MOUSE	O911f7 mus musculus
30	103.5	4.8	858	TUR5_HUMAN	O60602 homo sapien
31	103	4.8	365	CXAR_HUMAN	P78310 homo sapien
32	102.5	4.8	802	TUR4_HUMAN	P22485 homo sapien
33	100.5	4.7	629	YS50_MYCTU	O05809 mycobacteri

34	100	4.7	1032	1	TUR8_MOUSE	P58682 mus musculus
35	98	4.6	811	1	TUR4_HUMAN	O94xrs homo sapien
36	98	4.6	1032	1	TUR9_MOUSE	O94eq3 mus musculus
37	98	4.6	1041	1	TUR8_HUMAN	O94r97 homo sapien
38	96.5	4.5	766	1	SW7_BRARE	O94hxx4 brachydanio
39	96	4.5	288	1	PH22_MOUSE	O94dc6 mus musculus
40	95	4.4	676	1	LX1B_HUMAN	O15296 homo sapien
41	94	4.4	2012	1	DISCA_HUMAN	O60469 homo sapien
42	93.5	4.4	1709	1	SN_HUMAN	O94pzz2 homo sapien
43	93	4.3	764	1	ICCR_DROME	O08180 drosophila
44	92	4.3	729	1	AD21_MOUSE	O91176 mus musculus
45	92	4.3	1694	1	SN_MOUSE	O62230 mus musculus

ALIGNMENTS

```

RESULT 1
ID IL1R_HUMAN
AC P14778:
DT 01-APR-1990 (rel. 14, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Interleukin-1 receptor, type I precursor (IL-1R-1) (IL-1R-alpha)
DE (P80) (Antigen CD121a).
GN IL1R1 OR IL1RA OR IL1R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBT_Taxid-9606;
[1]
RP TISSUE=Liver;
RX MEDLINE=90098789; PubMed=2532321;
RA Chua A.O., Gubler U.;
RT "Sequence of the cDNA for the human fibroblast type Interleukin-1
RT receptor."
RL Nucleic Acids Res. 17:10114-10114(1989).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=T-cell;
RX MEDLINE=90046906; PubMed=2530587;
RA Sims J.E., Acres R.B., Gubler C.E., McMahon C.J., Wignall J.M.,
RA March C.J., Dower S.K.;
RT "Cloning the Interleukin 1 receptor from human T cells."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8946-8950(1989).
[3]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 18-332 IN COMPLEX WITH IL1B.
RX MEDLINE=97215903; PubMed=9062193;
RA Vigers G.P., Anderson I.J., Caffes P., Brandhuber B.J.;
RT "Crystal structure of the type-I Interleukin-1 receptor complexed
RT with Interleukin-1beta."
RL Nature 386:190-194(1997).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 21-331 IN COMPLEX WITH IL1RA.
RX MEDLINE=97215904; PubMed=9062194;
RA Scharf H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT "A new cytokine-receptor binding mode revealed by the crystal
RT structure of the IL-1 receptor with an antagonist."
RL Nature 386:194-200(1997).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO
CC THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD121a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd121a.htm".
CC -----
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[illegible]

Db 439 VINENKKSRRLILIVRETSGEFMGSGSEEDLAWNNALVQDGKIVLLELEKTIQYEK 438

OY 255 RPLFTFEQGRDPMRALRLROHRLVTLIL-----RPGSVTSSDPKKEVQLALP 308

Db 499 MPSTLFIKOK-----HGAIL-----WSGDPFQGGQSKATRTKNNVRRHNE 539

ID	IL1R_MOUSE	STANDARD:	PT:	576 AA.
AC	PI3504;			
DT	01-JUN-1990 (Rel. 13, Created)			
DT	01-JUN-1990 (Rel. 13, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-1 receptor, type I precursor (IL-1R-1) (P80).			
EN	IL1R1 OR IL1RA OR IL-1RL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId:10090;			
RN	[1]			
RX	SEQUENCE FROM N.A., AND SEQUENCE OF 20-45.			
RA	MEDLINE=88290679; PubMed=2969618;			
RA	Sims J.E., March C.J., Cosman D., Widmer M.B., McDonald H.R.,			
RA	McManan C.J., Grubin C.E., Mignall J.M., Jackson J.L., Call S.M.,			
RA	Friend D., Albert A.R., Gillis S., Urdal D.L., Dower S.K.,			
RT	"CDNA expression cloning of the IL-1 receptor, a member of the			
RT	immunoglobulin superfamily."			
RL	Science 241:585-589(1988).			
RN	[2]			
RP	PHOSPHORYLATION AT THR-556			
RP	MEDLINE=91254338; PubMed=1828344;			
RA	Bird T.A., Woodward A., Jackson J.L., Dower S.K., Sims J.E.;			
RT	"Photol ester induces phosphorylation of the 80 kilodalton murine			
RT	Interleukin 1 receptor at a single threonine residue."			
RL	Biochem. Biophys. Res. Commun. 177:61-67(1991).			
CC	-1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),			
CC	AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO			
CC	THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.			
CC	-1- SUBCELLULAR LOCATION: type 1 membrane protein.			
CC	-1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	-1- SIMILARITY: CONTAINS 1 TIR DOMAIN.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: M20658; AAA39279.1; -			
DR	PIR: A32604; A32604.			
DR	HSP: P14778; 11R.			
DR	MCD; MG1:96545; 11R1.			
DR	Interpro: IPR003006; I9_MHC.			
DR	Interpro: IPR003600; I9_1ike.			
DR	Interpro: IPR004076; InIL1k1_receptor1_pre.			
DR	Interpro: IPR004075; InIL1knl_receptor1.			
DR	Interpro: IPR004074; InIL1knl_receptor1_II.			
DR	Interpro: IPR000157; TIR.			
DR	Pfam: PF00047; I9; 2.			
DR	Pfam: PF01582; TIR; 1.			
DR	PRINTS: PRO1538; INTERLEUKN1R1.			
DR	PRINTS: PRO1536; INTERLEUKN1R2F.			
DR	PRINTS: PRO1537; INTERLEUKN1R1F.			
DR	SMART: SM00410; IG_1ike; 1.			
DR	SMART: SM00255; TIR; 1.			
DR	PROSITE: PS50104; TIR; 1.			
DR	Immunoglobulin domain: Receptor; Glycoprotein; Transmembrane; Signal;			
KW	Repeat, Phosphorylation.			
FT	SIGNAL 1			
FT	CHAIN 20 576 INTERLEUKIN-1 RECEPTOR, TYPE I.			

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FT DOMAIN 20 338 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 339 359 POTENTIAL.
FT DOMAIN 360 576 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 113 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 138 206 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 244 322 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 386 344 TIR.
FT DISULFID 25 107 BY SIMILARITY.
FT DISULFID 46 99 BY SIMILARITY.
FT DISULFID 145 199 BY SIMILARITY.
FT DISULFID 251 315 BY SIMILARITY.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 PHOSPHORYLATION (BY PC).
SC SEQUENCE 576 AA: 66697 MW: 7AA8304C86412A16 CRC64:

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Query Match 8.9% Score 190.5; DB 1; Length 576;
Best Local Similarity 24.0%; Pred. No. 1.1e-08;
Matches 86; Conservative 71; Mismatches 151; Indels 51; Gaps 18;

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QY 6 DRAPDLSPSDQVLRPALGSSVALNCTAMVVSQPHCSLPYQVLMKGLPLIGHYSLH 65
DB 227 DR-PVLSR-RNETIADSGMIQLCN--VTGQSDL-VYMKNGSIEMNDFLAE 279
QY 66 EYSWK--ANLSEVLYSVLVGNVSTEVYQ-AFTCSIONIS-FSSFTLQACPTSHVA 121
DB 280 DVQFVHPSTKRYTLITLNLISEVKSQFYRPFICVNVNMFESAHVOLLTPVDFKN 339
QY 122 VLASLLVL--ALLAALLVYKCRNLVLMYDA--YGEVLENDKRIYDAVY----- 169
DB 340 YLIGGTLITATIVCCVCYIKFKVDIVLMYRSCGSLPSKSDSKYDAYLYPKTIG 399
QY 170 --SYSDPEDRKVFNLKPOLERRRGYKFLDRLPRAEPSADLLVLSRCRLIYV 227
DB 400 EGSFSLD--TFVFKLLEVELEGQGYKFLFYGRDQYGEDEVTEVNEVKKSRLLII 456
QY 228 LSAFSLRAMCSIFREGICRLLELTRPFTF---EGQRDPAPALRLRLRQRLHY 283
DB 457 LVARDMGFSLMGSSSEQALVYNALIQEGIKVLELEKIKQDEKAPDSIOFTKQ-KHGV 515
QY 284 TLLIW-----RPGSVTPSSDFKWEYQALLPKRV-----YRPEEDPQTQLODDKDP 331
DB 516 --ICWSGDFQERQSA--KTRFMKRLRYQMPAPQRSPLSKHRLLLDP--VADTKRKL 567

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RESULT 3
TOLL_DROME STANDARD; PRT: 1097 AA.
AC P08953; Q9YBB8;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Toll protein precursor.
GN TL OR G55490.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8135760; PubMed=2449285;
RA Hashimoto C., Hudson K.L., Anderson K.V.;
RT "The Toll gene of Drosophila, required for dorsal-ventral embryonic
RT polarity, appears to encode a transmembrane protein."
RL Cell 52:269-279(1988).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Milos G.L.G.,
RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svitzkas R., Tector C., Turner R., Venter L., Venter A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster."
RN Science 287:2185-2195(2000).
RN [3]
RP FUNCTION.
RX MEDLINE=91092252; PubMed=2124970;
RA Keith F.J., Gay N.J.;
RT "The Drosophila membrane receptor Toll can function to promote
RT cellular adhesion."
RL EMBO J. 9:4299-4306(1990).
CC -!- FUNCTION: REQUIRED FOR DORSAL-VENTRAL EMBRYONIC POLARITY. MAY
CC -!- FUNCTION AS A MEMBRANE RECEPTOR. PROMOTES HETEROPHILIC CELLULAR
CC ADHESION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS 1 TIR DOMAIN.
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CC or send an email to license@sib-sib.ch).
DR EMBL: M19669; AAA28941.1; -
DR EMBL: AE003758; AAF56624.1; -
DR PIR: A28943; A28943.
DR Flybase: FBgn0003717; TL.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR-Clterm.
DR InterPro: IPR000372; LRR-Nterm.
DR InterPro: IPR003592; LRR-out.
DR InterPro: IPR003591; LRR-tyr.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR; 11.

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DR Pfam; PF01463; LRCT; 2.
DR Pfam; PF01462; LRNT; 1.
DR Pfam; PF01582; TIR; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00082; LRCT; 2.
DR SMART; SM00013; LRNT; 1.
DR SMART; SM00369; LRR_TYF; 3.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Developmental protein; Transmembrane; Glycoprotein; Repeat;
Cell adhesion; Leucine-rich repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 1097
FT DOMAIN 28 807
FT TRANSMEM 808 828
FT DOMAIN 829 1097
FT REPEAT 149 172
FT REPEAT 174 195
FT REPEAT 196 219
FT REPEAT 221 243
FT REPEAT 245 267
FT REPEAT 268 291
FT REPEAT 293 317
FT REPEAT 319 340
FT REPEAT 341 364
FT REPEAT 365 388
FT REPEAT 390 412
FT REPEAT 413 436
FT REPEAT 438 459
FT REPEAT 472 495
FT REPEAT 521 546
FT REPEAT 550 574
FT REPEAT 667 690
FT REPEAT 692 713
FT REPEAT 714 736
FT REPEAT 785 807
FT DOMAIN 857 996
FT CARBOHYD 80 140
FT CARBOHYD 140 175
FT CARBOHYD 235 270
FT CARBOHYD 270 275
FT CARBOHYD 346 391
FT CARBOHYD 391 482
FT CARBOHYD 482 508
FT CARBOHYD 508 528
FT CARBOHYD 528 654
FT CARBOHYD 654 677
FT CARBOHYD 677 702
FT CARBOHYD 702 715
FT CARBOHYD 715 730
FT CARBOHYD 730 738
FT CARBOHYD 738 738
SQ SEQUENCE 1097 AA; 124655 MW; D1BFC42245E3EABE C664;

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Query Match 8.28; Score 176; DB 1; Length 1097;
 Best Local Similarity 25.78; Pred. No. 4; 8e-07;
 Matches 70; Conservative 47; Mismatches 89; Indels 66; Gaps 13;

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OY 121 AVLSLVLALLLALLLY-----VKRL-----AVLWYQDAYGEVLENDCKLYDAYYSV 172
DB 810 AVVLAITGLGFTALTYKFTQTEIKIWLVAHNLMLP-----VTEEDIDKKKFDALFISV 866
OY 173 DCPEDRKVFNLKPQLEIR-RRGYKFLDRLDLPRAEPSADLLVNLRCRLIIVLSDA 231
DB 867 H-KDQSFIEIYLVPOLEHGPOKFOLCVHERDWLVGCHIEENIMRSVADSRRTIIVLSON 924
OY 232 FLRWASCSHSFR-----EGLCRLLELTRRPIFITFEQGRDPAPRALRLRQHRLV 283
DB 925 FIKSEWALFERAHRARSALNCGRSRTIIVTYSDI---GDVEKLDEE-----LKAVLKMN 975

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OY 284 TILLMRPGSVTPSSD--FWKEVQALPKRVRYRPEGDPOTODDKDMLILRGVPEG 341
DB 976 TYLKW-----GDPWFWDKIRFALPHR-----RPV-----GNINGC 1005
OY 342 RALDEVDPDPEGDGVGRPVFGESAPPHVS 373
DB 1006 ALIKTALKGSTDKLELIK-----SPVTPPLTT 1034

RESULT 4
ILIR_RAT
ID ILIR_RAT STANDARD; PRT; 576 AA.
AC 002955;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type I precursor (IL-1R-1) (P80).
GN ILIR1 OR ILIRa.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ganglion;
RX MEDLINE=93266794; PubMed=7684399;
RA Hart R.P., Liu C., Shadlack A.M., McCormack R.J., Jonakait G.M.;
RT "An mRNA homologous to interleukin-1 receptor type I is expressed in
RT cultured rat sympathetic ganglia."
RL J. Neuroimmunol. 44:49-56(1993).
CC -! FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -! SIMILARITY: CONTAINS 1 TIR DOMAIN
CC -----
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CC -----
DR EMBL; M95578; AAA16196.1; ALT_SEQ.
DR HSSP; P14778; ILIRa.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR004076; ILIR1_receptor_pre.
DR InterPro; IPR004075; ILIR1_receptor.
DR InterPro; IPR004074; Intriknl_receptor.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01538; INTRLEUKN1R1.
DR PRINTS; PR01537; INTRLEUKN12F.
DR PRINTS; PR01537; INTRLEUKN1R1F.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
KW Repeat; Phosphorylation.
FT SIGNAL 1 19
FT CHAIN 20 576
FT DOMAIN 20 338
FT TRANSMEM 339 359
FT DOMAIN 360 576
FT DOMAIN 39 113
FT DOMAIN 138 206
FT DOMAIN 244 322
FT DOMAIN 386 544
FT DISULFID 25 107
BY SIMILARITY.

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Db 647 VGVGLVVKFYHMLMLLCKCKKRGGE-----SIIDAFVIYS--QDDDWNRNEIVKLEEG 700
Oy 192 RRGKFLFDRLDRLPRAPPSADL-VNLSCKRLIYVLSDFLSRWKSHSF-----242
Db 701 VPPOLCLHRDFTPGVAIANITIGEGHRSRKVIYVSOHFQSRWCIFEEYIAQTWOF 760
Oy 243 ---REGICRLLELTRRPDIFTFEGQRRDPAPALRLRQHRMLV-----TLLMRPGSV 293
Db 761 LSSAGI-----IFVLCKLEKS-----LIRQOVELYRLLSRNTYLEWE-DSV 802
Oy 294 TPSSDFKEVOLAPRKRYRYPVEGDPOTQLODDKPMILRGRVPEGRALSEVDP 350
Db 803 LGRHVFWRRLRKAL-----LAGKPOQ-----PEGTA-DAETNP 834

```

RESULT 6

TLR2_MOUSE STANDARD: PRT: 784 AA.

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ID TLR2_MOUSE
AC OQUNT: 09DEC4:
DP 01-MAR-2002 (Rel. 41, Created)
F 01-MAR-2002 (Rel. 41, Last sequence update)
L 01-MAR-2002 (Rel. 41, Last annotation update)
DE TOLL-like receptor 2 precursor.
GN TLR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF PRO-681.
RX MEDLINE=20014145; Pubmed=10548109;
RA Underhill D.M., Ozinsky A., Hajjar A.M., Stevens A., Wilson C.B.,
RA Bassett M., Aderem A.;
RT "The TOLL-like receptor 2 is recruited to macrophage phagosomes and
RL discriminates between pathogens."
RL Nature 401:811-815(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=99288048; Pubmed=10358136;
RA Heine H., Kirschning C.J., Lien E., Monks B.G., Rothe M.,
RA Cohen P.D.T.;
RT "Cutting edge: cells that carry a null allele for TOLL-like receptor 2
RT are capable of responding to endotoxin."
RL J. Immunol. 162:6971-6975(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX Pubmed=10666214;
RA Matsunuchi T., Takagi K., Musikacharen T., Yoshikai Y.;
RT "Gene expressions of lipopolysaccharide receptors, TOLL-like
RT 2 and 4, are differentially regulated in mouse T lymphocytes."
RL Blood 95:1378-1385(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipocyte;
RX Pubmed=10823826;
RA Lin Y., Lee H., Berg A.H., Lisanti M.P., Shapiro L., Scherer P.E.;
RT "The lipopolysaccharide-stimulated TOLL-like receptor (TLR)-4 induces
RT synthesis of the closely related receptor TLR-2 in adipocytes."
RL J. Biol. Chem. 273:24253-24263(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koshiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nakano I., Pesole G., Quackenbush J.,

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RA Schriani L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Cooperates with MD-2 and TLR6 to mediate the innate
CC immune response to bacterial lipoproteins and other microbial cell
CC wall components. Acts via MyD88 and TRAF6 leading to NF-kappa-B
CC activation, cytokine secretion and the inflammatory response. May
CC also promote apoptosis in response to lipoproteins (By
CC similarity).
CC -1- SUBUNIT: Binds MD-2 and TLR6 via the extracellular domain. Binds
CC MyD88 via their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosome.
CC -1- TISSUE SPECIFICITY: Detected in a macrophage cell line, smooth
CC muscle, lung, spleen, thymus, brain and adipose tissue.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -1- SIMILARITY: CONTAINS 16 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL: AF185284; AAF04277.1; -
DR EMBL: AF124741; MAD6481.1; -
DR EMBL: AF216283; AAF28345.1; -
DR EMBL: AF165189; AAD48335.1; -
DR EMBL: AK005043; BAB23770.1; -
DR WGD; MG1:1346060; TLR2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR: 6.
DR Pfam: PF01582; TIR: 1.
DR PRINTS: PR00019; LEURICRPT.
DR SMART: SM00370; LRR: 1.
DR SMART: SM00082; LRRCT: 1.
DR SMART: SM00369; LRR_TYR: 2.
DR SMART: SM00255; TIR: 1.
DR PROSITE: PS0104; TIR: 1.
KM Receptor: Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT STGNAL 1 24
FT CHAIN 25 784
FT DOMAIN 25 587
FT TRANSMEM 588 608
FT DOMAIN 609 784
FT REPEAT 51 74
FT REPEAT 75 98
FT REPEAT 99 122
FT REPEAT 124 147
FT REPEAT 173 196
FT REPEAT 221 244
FT REPEAT 276 300
FT REPEAT 335 358
FT LRR 8.

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FT REPEAT 359 384 LRR 9.
 FT REPEAT 386 411 LRR 10.
 FT REPEAT 412 436 LRR 11.
 FT REPEAT 438 456 LRR 12.
 FT REPEAT 457 476 LRR 13.
 FT REPEAT 477 500 LRR 14.
 FT REPEAT 502 521 LRR 15.
 FT REPEAT 522 548 LRR 16.
 FT DOMAIN 137 784 TIR.
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 681 681 P->H: ABOLISHES MYD88-BINDING AND RESPONSE TO MICROBIAL CELL WALL COMPONENTS.
 FT CONFLICT 59 59 L->P (IN REF. 5).
 FT CONFLICT 82 82 I->M (IN REF. 5).
 SO SEQUENCE 784 AA; 89448 MM; 606D56BF85F320A2 CAC64.
 Best Local Similarity 25.1%; Score 144; DB 1; Length 784;
 Matches 74; Conservative 41; Mismatches 114; Indels 66; Gaps 12.
 Try Match 6.7%;
 QY 72 ANLSEVLVSSVLGVAVVST-----EYGA-----FICSTONISFSST----- 109
 Db 495 ASLFVLLVLMKIRENAVSTFSKQDGSFPEKLETLBAGDNHFVCSCELLSFMTETPALAOI 554
 OY 110 -----LORAGPT---SHVAVLAST---LVLLDLALLLVKCR 143
 Db 555 LVDMEDSTLCSPPRLHGHRLDADAPSVLECHQALVSGVCCALLLLLVGL-----CH 610
 QY 144 LNVLLWY---ODAYGEVEINDGK-----LYDAVVSYSDCPEDEKRFVFTLKPOLERR-R 193
 Db 611 HPHGMLTVLRMMWAMIQAKRKPKACRQDVCDAFYVSYSE--QDSHWENVLWVQLENSDP 668
 QY 194 GYKLLDDROLLPRAEPESADLLVNSRCRLIVYLSDAFLSNACSHSREBELCYLL-EL 252
 Db 669 PEKLLHMRDPEFGKWIIDNIISIEKSHKTVFVLENFRESEKCYELDFSHFLPFDEN 728
 QY 253 TRRPFIFFEGORPAPRALRLHQRHRLVLLLMRPGSVTPSSDMEKREYOLAL 307
 Db 729 NDAIVLLLEPIERKAIPORFCKLKRKIMNTKTYLEM-PLDESGQOEYFVNVNTRAI 782
 RESULT 7
 TLR4.PAPAN STANDARD: PRT: 826 AA.
 1 TLR4.PAPAN
 2 09TSP2:
 3 01-MAR-2002 (Rel. 41, Created)
 4 01-MAR-2002 (Rel. 41, Last sequence update)
 5 01-MAR-2002 (Rel. 41, Last annotation update)
 6 Toll-like receptor 4 precursor.
 7 TLR4.
 8 Paplo anubis (Olive baboon).
 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 10 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 11 Cercopithecinae; Papio.
 12 NCBI_TaxID=9555;
 13 [1]
 14 SEQUENCE FROM N.A.
 15 PubMed=11104518;
 16 Smirnova I., Poltorak A., Chan E.K.T., McBride C., Beutler B.;
 17 "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 18 locus (TLR4).";
 19 (In) Genome Biol. 1:RESEARCH002.1-2.10(2000).
 20 -I- FUNCTION: Cooperates with MD-2 and CD14 to mediate the innate
 21 immune response to bacterial lipopolysaccharide (LPS). Acts via
 22 MYD88, TIRAP and IRAF6, leading to NF-kappa-B activation, cytokine
 23 secretion and the inflammatory response (By similarity).
 24 -I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 25 multi-protein complex containing at least CD14, MD-2 and TLR4.
 26 Binds MD-2 via the extracellular domain. Binds MYD88 and TIRAP via
 27 their respective TIR domains (By similarity).

[illegible]

01-MAR-2002 (rel. 41, last annotation update)
 Toll-like receptor 4 precursor.
 GN TLR4.
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9597;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11104518;
 RA Smithova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 locus (TLR4)."
 RL (in) Genome Biol. 1:RESEARCH002.1-2.10(2000).
 CC -1- FUNCTION: Cooperates with MD-2 and CD14 to mediate the innate
 immune response to bacterial lipopolysaccharide (LPS). Acts via
 MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 multi-protein complex containing at least CD14, MD-2 and TLR4.
 CC Binds MD-2 via the extracellular domain. Binds MyD88 and TIRAP via
 their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC -1- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
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 CC -----
 DR EMBL: AF179220; AAF05320.1; -.
 DR EMBL: AF179218; AAF05320.1; JOINED.
 DR EMBL: AF179219; AAF05320.1; JOINED.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00560; LRR: 9.
 DR Pfam: PF01463; LRRCT: 1.
 DR Pfam: PF01582; TIR: 1.
 DR PRINTS: PRO00019; LEORICHRPT.
 DR SMART: SM00370; LRR: 2.
 DR SMART: SM00082; LRRCT: 1.
 DR SMART: SM00369; LRR_Typ: 2.
 DR SMART: SM00255; TIR: 1.
 DR PROSITE: PS50104; TIR: 1.
 DR Receptor; Immune response; Inflammatory response; Signal;
 KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 839
 FT DOMAIN 24 631
 FT TRANSMEM 632 652
 FT DOMAIN 633 839
 FT REPEAT 52 76
 FT REPEAT 77 100
 FT REPEAT 101 124
 FT REPEAT 128 149
 FT REPEAT 150 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 228 252
 FT REPEAT 277 303
 FT REPEAT 307 330
 FT REPEAT 332 350
 FT REPEAT 351 372
 FT REPEAT 373 398
 FT REPEAT 400 421
 LRR 14.

FT REPEAT 422 445 LRR 15.
 FT REPEAT 447 469 LRR 16.
 FT REPEAT 470 494 LRR 17.
 FT REPEAT 495 518 LRR 18.
 FT REPEAT 520 541 LRR 19.
 FT REPEAT 543 566 LRR 20.
 FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818
 FT CARBOHYD 35 35
 FT CARBOHYD 173 173
 FT CARBOHYD 205 205
 FT CARBOHYD 282 282
 FT CARBOHYD 309 309
 FT CARBOHYD 497 497
 FT CARBOHYD 526 526
 FT CARBOHYD 575 575
 FT CARBOHYD 624 624
 FT CARBOHYD 630 630
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;
 Query Match 5.2%; Score 134; DB 1; Length 839;
 Best Local Similarity 22.7%; Pred. No. 0.0014;
 Matches 78; Conservative 59; Mismatches 116; Indels 91; Gaps 15;
 DB 11 FLSPSEDOVLRPALGSSVALNCTAWVSGPHCSLPVQWIKDGLPIGIGHSLSHEYSW 70
 516 FNLSSIQVLNMSHNNFFSID-----TPPYKCLNSIQVL-----DYLNIHMTS 559
 QY 71 KANLSEVLVSSVGLVNTSTEVYGAFTCSIONISFSF-----TIQAGPTG- 117
 DB 560 KQELQHPFSLSAFLNLTQND---FACTEHQSFQWIKDQQLVEVERMCCAPPSDK 615
 QY 118 -----HAAVLASLLVLLALLLALVYKCLANVLWQDXYGVEIENDK 163
 DB 616 QGMPVLSLNTTCQMNKTITIGSVLSVLSVAVLVYKFFHML-----LAGCIKGRGE 671
 QY 164 -LYDAVSYSDCPEDRKFV-NFLTKPOLERRRGYKFLIDRDLLPRAEPSADLL-VNLSR 220
 DB 672 NIYDAVIYSS--QDEDMVNLKYLEGVPFQCLHREDIPGVAIAANIHEGFHK 729
 QY 221 GRRLIVLSDAFLSRWCSHSF-----REGICRLLELTRRPIFTFEGQRDPA 269
 DB 730 SRKVIYVVSQHFQSRWCIREYEIACTWQFLSSRAGI-----IFVLQVKER--- 776
 QY 270 HPAALRLRQHRHLV-----TLLMRGSGYTPSSDPFKEVQAL 307
 DB 777 ----TLRQVELYRLLSRNTYLEWE-DSVLGRHITWRRLKAL 815
 RESULT 12
 ID TL22_CHICK STANDARD; PRT; 781 AA.
 AC Q9DGB6;
 DT 01-MAR-2002 (rel. 41, Created)
 DT 01-MAR-2002 (rel. 41, last sequence update)
 DE 01-MAR-2002 (rel. 41, last annotation update)
 GN TLR2-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX PubMed=11590137;
 RA Fukui A., Inoue N., Matsumoto M., Nomura M., Yamada K., Matsuda Y.,
 RA Toyoshima K., Seya T.;
 RT "Molecular cloning and functional characterization of chicken
 Toll-like receptors, a single chicken Toll covers multiple molecular
 patterns.";
 RT J. Biol. Chem. 276:47143-47149(2001).

```
CC -1- FUNCTION: Participates in the innate immune response to microbial
CC agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B
CC activation, cytokine secretion and the inflammatory response.
CC Mediates the response to mycoplasma macrophage-activating
CC lipopeptide-2kD (MALP-2).
CC SUBUNIT: Binds MyD88 via their respective TIR domains. Binds TR6
CC via their respective extracellular domains (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in ovary. Also detected in
CC brain, heart, lung, liver, spleen and kidney, and at low levels in
CC placenta, muscle, testis and proventriculus.
CC -1- PMW: N-61 kDa.
CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -1- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
CC -----
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```

DR EMBL: AB046533; BAB16842.1; -
DR InterPro: IPR001611; LRR
DR InterPro: IPR000483; LRR, C-term.
DR InterPro: IPR003592; LRR, out.
DR InterPro: IPR003591; LRR, Lyp.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR; 9.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR00019; LEURICRPT.
DR SMART: SM00370; LRR; 5.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00369; LRR, TYP; 7.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR Receptor: Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 781
FT DOMAIN 25 781
FT TRANSMEM 585 585
FT DOMAIN 606 606
FT DOMAIN 607 781
FT REPEAT 51 74
FT REPEAT 75 98
FT REPEAT 100 122
FT REPEAT 124 147
FT REPEAT 148 171
FT REPEAT 173 195
FT REPEAT 195 381
FT REPEAT 356 381
FT REPEAT 383 409
FT REPEAT 410 433
FT REPEAT 435 453
FT REPEAT 454 473
FT REPEAT 474 497
FT REPEAT 499 518
FT DOMAIN 636 781
FT CARBOHD 37 109
FT CARBOHD 109 150
FT CARBOHD 150 184
FT CARBOHD 184 301
FT CARBOHD 301 313
FT CARBOHD 313 333
FT CARBOHD 330 390
FT CARBOHD 439 439
SO SEQUENCE 781 AA; 89094 MW; 7211B399C6320454 CRC64;

Query Match Best Local Similarity 23.6%; Score 131; DB 1; Length 781; Matches 60; Conservative 37; Mismatches 109; Indels 48; Gaps 9;

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OY 96 FTCSIONISFSSTLORAG-----PTSHA-----AVLA 124
DB 532 FICSE---FISFHHNGEAGVLGVWPESTICSPITRGAGVGYOLSLMECHRSLL 588
OY 125 SLVLALLALLAALLVYKRLNLLWYOD---AGEVEINDEK-----LVDAYVYSDCP 175
DB 589 SLICLVLFFELILLVVGKYKHAWMYMTWMLQAKRKPRAPTKDICYDAFVYSE--646
OY 176 EERKRVYTLKQLEERR-RGKRLFLDRDLPRAPESADLLVNSRCRLIVLSDAFLS 234
DB 647 NDSNWEVNIWQOLEQACRPRLCLHKRDVPYGVWYDNIIDSTIEKSHKTLFVLSHFVQ 706
OY 235 RAMCHSRFBEGICRL-LTRRPPIFTFGORNDPAHRLRLRQNRHVTLLMPGCV 293
DB 707 SEMKYEIDFHFHFLDENNDVALILLLEPIQSQATPRKCKLRKIMNTKTYLEMPDE-765
OY 294 TPSSDFKVEYQAL 307
DB 766 FQQGMFWENIKKAL 779
```

RESULT 13

ID	TLR2_MACFA	STANDARD	PRT	784 AA
AC	O95M53			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Toll-like receptor 2 precursor.			
GN	TLR2.			
OS	Macaca fascicularis (Crib eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Monocytes;			
RA	Roberts F.A., Tang S.;			
RT	Macaca fascicularis Toll-like Receptor 2.;			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBP databases.			
CC	-1- FUNCTION: Cooperates with MD-2 and TIR6 to mediate the innate			
CC	immune response. Acts via MyD88 and TRAF6, leading to NF-kappa-B			
CC	activation, cytokine secretion and the inflammatory response. May			
CC	also promote apoptosis in response to lipopeptides (by			
CC	similarity).			
CC	-1- SUBUNIT: Binds MD-2 and TIR6 via the extracellular domain. Binds			
CC	MyD88 via their respective TIR domains (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).			
CC	-1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 TIR DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement. (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: AY045573; AAR91868.1; -			
DR	PROSITE: PS50104; TIR; 1.			
KW	Receptor; Immune response; Inflammatory response; Signal;			
KW	Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.			
FT	SIGNAL 1 18			
FT	CHAIN 19 784			
FT	DOMAIN 19 587			
FT	TRANSMEM 588 588			
FT	DOMAIN 609 784			
FT	REPEAT 51 74			
	LRR 1.			

RESULT 14	TL21_CHICK	STANDARD;	PRT;	793 AA.
ID	TL21_CHICK			
AC	09DD78;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Toll-1-like receptor 2 type 1 precursor.			
GN	TLR2-1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	PubMed-11590137;			
RA	Fukui A., Inoue N., Matsumoto M., Nomura M., Yamada K., Matsuda Y.,			
RT	Tokushima K., Soga T.;			
RT	"Molecular cloning and functional characterization of chicken			
RT	Toll-1-like receptors. A single chicken Toll covers multiple molecular			
RT	patterns.";			
RT	J. Biol. Chem. 276:47143-47149(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Takahashi T.;			
RT	"Molecular cloning and expression analysis of the chick Toll-1-like			
RT	receptor 2 in embryonic ventricular myocytes.";			
RT	Submitted (JUL-2000) to the EMBL/Genbank/DBD databases.			
CC	-1- FUNCTION: Participates in the innate immune response to microbial			
CC	agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B			

DR	EMBL; AB050005; BAB16843.1; -.
DR	EMBL; AB046119; BAB16113.2; -.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR003592; LRR_Out.
DR	InterPro; IPR003591; LRR_Typ.
DR	InterPro; IPR000157; TIR.
DR	Pfam; PF00560; LRR; 4.
DR	Pfam; PF01463; LRCT; 1.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR00019; LEURICHRPT.
DR	SMART; SMO0370; LRR; 4.
DR	SMART; SMO0082; LRCT; 1.
DR	SMART; SMO0369; LRR_Typ; 6.
DR	SMART; SMO0255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KW	Receptor; Immune response; Inflammatory response; Signal;
KW	Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT	SIGNAL 1 25 POTENTIAL.
FT	CHAIN 26 793 TOLL-LIKE RECEPTOR 2 TYPE 1.
FT	DOMAIN 26 597 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 598 618 POTENTIAL.
FT	DOMAIN 619 793 CYTOPLASMIC (POTENTIAL).
FT	REPEAT 62 85 LRR 1.
FT	REPEAT 86 109 LRR 2.
FT	REPEAT 111 133 LRR 3.
FT	REPEAT 135 158 LRR 4.
FT	REPEAT 159 182 LRR 5.
FT	REPEAT 184 206 LRR 6.
FT	REPEAT 344 370 LRR 7.
FT	REPEAT 395 419 LRR 8.
FT	REPEAT 421 445 LRR 9.
FT	REPEAT 447 465 LRR 10.
FT	REPEAT 466 485 LRR 11.
FT	REPEAT 486 509 LRR 12.
FT	REPEAT 511 530 LRR 13.
FT	DOMAIN 648 793 TIR.
FT	CARBOHYD 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE 793 AA; 90766 MW; 2BF5E9D9305D4562 CRC64;

Query Match 6.1%; Score 131; DB 1; Length 793;
Best Local Similarity 23.6%; Pred. No. 0.0023;
Matches 60; Conservative 37; Mismatches 109; Indels 48; Gaps 9;

QY 96 PFCSTONISSFTLORAG-----PISHVA-----AVIA 124
 DB 544 FISCSE---FLSFTIHAGIAOVLCVGPESYIDSLPLVGAOVGSVOLIMECHSLLV 600
 QY 125 SLVLALLALLAALVYKCRINVLWYOD---AYGEVEINDGK-----LYDAYVSYSDP 175
 DB 601 SLICTLWFLFLLLVVGYKYHAWYMTWMLQAKRKPRAPTRDIDICDAFVXSE-- 658
 QY 176 EDRKFEVFIKPOLERR-REGKFLDRLDLPRAEPSADLVNLSRCRLIVLSDAFLS 234
 DB 659 NDSMNWENIMVQOLEQACPFRLCLHNRDVPFGKWIYDNIIDISKSHTLFVLSHFVQ 718
 QY 235 RAMCSHFRGGLRL-ELTRRPFIETFEQGRDPAHAPALRLRHRHLVTLILMPGSV 293
 DB 719 SEMCKYELDSHRLFDENNDAVILILPILQSOAIPKRCCKLRKIMNTKTYLEMPDE- 777
 QY 294 TPSSDFWKEVOLAL 307
 DB 778 EQOQMFWENLKAL 791

TLR4_HORSE STANDARD: PRT: 843 AA.
 ID TLR4_HORSE
 AC G9WY3;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE TOLL-like receptor 4 precursor.
 GN TLR4.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vandeplass M.L., McNeill B.W., Barton M.H., Moore J.N.:
 RT Cloning and sequencing of equine toll-like receptor 4 (TLR4)."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with MD-2 and CD14 to mediate the innate
 immune response to bacterial lipopolysaccharide (LPS). Acts via
 MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 multi protein complex containing at least CD14, MD-2 and TLR4.
 CC Binds MD-2 via the extracellular domain. Binds MYD88 and TIRAP via
 their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC -1- SIMILARITY: CONTAINS 19 LEUCINE-RICH REPEATS (LRR).
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 CC
 DR EMBL: AY005808; AAF91076.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_Tyr.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00560; LRR_11.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PRO0019; LEURICHRPT.
 DR SMART: SM00370; LRR; 3.
 DR SMART: SM00082; LRRCT; 1.

DR SMART: SM00369; LRR_TYP; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS0104; TIR; 1.
 KW Receptor; Immune response; Inflammatory response; Signal;
 KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 843
 FT DOMAIN 24 633
 FT TRANSMEM 634 654
 FT DOMAIN 655 843
 FT REPEAT 53 76
 FT REPEAT 77 100
 FT REPEAT 101 124
 FT REPEAT 128 149
 FT REPEAT 150 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 277 300
 FT REPEAT 311 334
 FT REPEAT 351 373
 FT REPEAT 374 399
 FT REPEAT 401 422
 FT REPEAT 423 446
 FT REPEAT 447 470
 FT REPEAT 471 495
 FT REPEAT 496 519
 FT REPEAT 521 544
 FT REPEAT 545 566
 FT REPEAT 569 593
 FT DOMAIN 674 820
 FT CARBOHYD 35 35
 FT CARBOHYD 189 189
 FT CARBOHYD 205 205
 FT CARBOHYD 282 282
 FT CARBOHYD 295 295
 FT CARBOHYD 498 498
 FT CARBOHYD 527 527
 FT CARBOHYD 576 576
 FT CARBOHYD 626 626
 SEQUENCE 843 AA; 96495 MW; B5976898ADE77A69 CRC64;
 Query Match Best Local Similarity 22.08; Score 129; DB 1; Length 843;
 Matches 76; Conservative 49; Mismatches 113; Indels 108; Gaps 17;

QY 42 CSLPSVQWIK-----DGLPLGIGHSYLHEYSWKANLSEVLV-----SSV 82
 DB 518 CLPRLRLVNLMSHNNLFLDMLP-----YKPLHSIQIIDCSFNRIYAFKMOELOHPPSL 572
 QY 83 LGVNTSTVEYGAFTCSIONISF-----SFTLORAG-----PT 116
 DB 573 ASLINTOND---FACVCEYOSFLQWVKDQROLVEVEHLCAIPLQMRGMPVLGFNNAT 628
 QY 117 SHVAAVLAS---LVLALLAALVYKCRINVLWYODAYGEVEINDGKLYDAYVSYSD 173
 DB 629 COISITVIGGSVFSILMSVIAVLYKFFFLMLAGCKKRGGE---SIYDAFVYSS 684
 QY 174 CEDRKFEV-NFLTKQLERRRGYKFLDRLDLPRAEPSADLVNLSRCRLIVLSDA 231
 DB 665 -QDEEDWVRNELVKNLEBGVPPFQCLHTRDFIGVAIAANIIDEGHKSRYIVVSSH 742
 QY 232 FLSTRWCSHSF-----REGICRLLELTRRPFIETFEQGRDPAHAPALRLRHR 280
 DB 743 FLSRWNCIFEYELIAOTWQFLSSRAGI-----IFIYVHLKES-----LNRQV 765
 QY 281 HLV-----TLLMRPGSVTPSSDFWKEVOLALPRKRYRVEGDP 320
 DB 766 ELYRLNNTYLEME-DSVLRHITFWRLRNAL-----LDGKP 822

Search completed: November 7, 2002, 18:50:18
 Job time : 29 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 18:44:41 ; Search time 44 Seconds
(without alignments)
895.378 Million cell updates/sec

Title: US-09-598-443-2

Perfect score: 2147

Sequence: 1 MPGVCDRAPDFLSPEDQVL.....GSRNYSARTDFYCLVSKDDM 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequenced: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215.5	10.0	570	A57535	interleukin-1 recep
2	209.5	9.8	569	A36187	interleukin-1 rece
3	204	9.5	562	G02426	interleukin-1 rece
4	190.5	8.9	576	A32604	interleukin-1 rece
5	189.5	8.8	567	S29498	lymphocyte antigen
6	184	8.6	555	J01526	interleukin-1 rece
7	176	8.2	1097	A29943	Toll protein precu
8	168.5	7.8	590	I55526	interleukin-1 rece
9	163	7.6	247	S42633	Fit-1M protein - r
10	144.5	6.7	1385	T13887	tlr protein - fru1
11	139.5	6.5	1389	T13852	gene wheeler prote
12	128.5	6.0	169	I51903	type I interleukin
13	123	5.7	799	S18209	fibroblast growth
14	115	5.4	243	S11226	MyD88 protein - mo
15	114.5	5.3	786	T08664	Toll protein-like
16	113.5	5.3	1323	PN0568	connectin 3B - chi
17	111	5.2	26926	I38344	fibroblast growth
18	109.5	5.1	822	S19947	fibroblast growth
19	109.5	5.1	822	B49151	fibroblast growth
20	103	4.8	650	JC1450	fibroblast growth
21	102.5	4.8	818	JC4058	fibroblast growth
22	100.5	4.7	629	E70589	protoporphyrin IX
23	99	4.6	379	G96754	hypothetical prote
24	98	4.6	363	B96754	Similar to part of
25	97	4.5	176	E96754	Similar to downy m
26	97	4.5	829	JC4583	fibroblast growth
27	96.5	4.5	380	C96734	Similar to part of
28	96.5	4.5	802	TVH0F4	fibroblast growth
29	95	4.4	815	T41490	hypothetical prote

30	94.5	4.4	411	2	T35102	probable transmemb
31	94.5	4.4	1024	2	G71434	probable limonene
32	94	4.4	1896	2	T08851	Down syndrome cell
33	93.5	4.4	275	2	D96754	Similar to part of
34	93.5	4.4	1179	2	T04584	TMV resistance pro
35	93.5	4.4	1344	2	T14316	rig-1 protein - hu
36	93.5	4.4	7962	2	I38346	elastic titlin - hu
37	93	4.3	764	2	A49448	irregular chiasm c
38	92.5	4.3	371	2	F96754	Similar to NL27 (i
39	92.5	4.3	2783	2	T34416	hypothetical prote
40	92	4.3	871	1	I48696	protein-tyrosine k
41	92	4.3	881	1	I48697	protein-tyrosine k
42	92	4.3	1694	2	S50065	protein-tyrosine k
43	92	4.3	1694	2	S50065	sialoadhesin - mou
44	91.5	4.3	357	1	C96695	ribulose biphosph
45	91.5	4.3	1039	2	A85096	transforming prote
						hypothetical prote

ALIGNMENTS

RESULT 1
A57535
interleukin-1 receptor accessory protein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C:Accession: A57535
R:Greenfeder, S.A.; Nunes, P.; Kwee, L.; Labow, M.; Chizzonite, R.A.; Ju, G.
J. Biol. Chem. 270, 13757-13765, 1995
A:Title: Molecular cloning and characterization of a second subunit of the interleukin
A:Reference number: A57535; MUID:95293970
A:Accession: A57535
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <GRE>
A:Cross-references: GB:985999; NID:9887520; PIDN:CAA59991.1; PID:9887521
A:Superfamily: interleukin-1 receptor type I
C:Keywords: transmembrane protein

Query Match 10.0%; Score 215.5; DB 2; Length 570;
Best Local Similarity 25.6%; Pred. No. 4.7e-10;
Matches 85; Conservative 61; Mismatches 153; Indels 33; Gaps 10;

QY	9	PDLFSPEDQVLKRALPAGSSVALNCTAW--VSGPHGSLPSYOMLKDG-LPLIGGHYSLH	65
DB	243	PQIYSNDRVYERKEPEGEELVLPCKYFSFINDSH---NEWMITDGKRPDDVTYDITIN	299
QY	66	EYSWVKNLSEVLVSVLGWNTSTEVGAFPCSION---ISFSSFTLQRRGP--TSH	118
DB	300	ESVSYSTEDERTFOILSTIKVTPEDLRNRYVCHARNTGAEAGQAKVAKVYIPRYTVE	359
QY	119	VAAVLASLVLALLALIAALLVYKRLNVLWTDAYGEVE-INDGKLAYAYVSYSCDPD	177
DB	360	LACGFCATFVLVAVL--VYHYHVMLEWLFYRAHGTDETLIDGKEXDIYVSARWEE	417
QY	178	RKRVNITLKPDERRRGYKFLPDDRPLRAEPSADLVNLSGCRILVYVLDAPFSRAW	237
DB	418	EEFVLLTLRGVLENERGYKLCIFDRSLDPGIVTDTLSFIQSRSLVLPSPNTV----	473
QY	238	CSHSFREGICRLLELTRRPIFTFEES-----QRRDPAHPALRLRQHRHVTLLMR-	289
DB	474	-----LQGNQALLELKAGLENNASRGINIVLVQYAAVDMKVKELKRAKYTLVTKMG	528
QY	290	PGSVTPSSDFKWEVOLALPRKYRYPVEDPQ	321
DB	529	EKSXPQGRFWKQLQVAMPVKRSPRWSNDKQ	560

RESULT 2
A36187
interleukin-1 receptor type I precursor - human
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 29-Sep-1999

C:Accession: A36187; S06928
 R:Stms, J.E.; Acres, R.B.; Gubin, C.E.; McKahan, C.J.; Wignall, J.M.; March, C.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8946-8950, 1989
 A:Title: Cloning the interleukin 1 receptor from human T cells.
 A:Reference number: A36187; MUID:90046906
 A:Accession: A36187
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-569 <SIM>
 R:Chna, A.O.; Gubler, U.
 Nucleic Acids Res 17, 10114, 1989
 A:Title: Sequence number of the cDNA for the human fibroblast type interleukin-1 receptor
 A:Reference number: S06928; MUID:90096789
 A:Accession: S06928
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-569 <CHN>
 A:Cross-references: EMBL:X16896; NID:933800; PIDN:CAA34773.1; PID:933801
 C:GeneID:3
 A:Gene: GDB:111R1; IL1RA; D2S1473; IL1R
 A:Cross-references: GDB:125254; OMTM:147810
 A:Position: 2912-2912
 C:Superfamily: Interleukin-1 receptor type I
 C:Keywords: cytokine receptor; transmembrane protein
 Query Match 9.8%; Score 209.5; DB 2; Length 569;
 Best Local Similarity 23.7%; Pred. No. 1.5e-09;
 Matches 85; Conservative 62; Mismatches 126; Indels 85; Gaps 16;
 Oy 7 RAPEFLSPEDQYLRPA-----LSSVALNCTAMVSGPHCLSPVQV---L 50
 Db 211 RVIEFTLEENKRTREVIASPANETMEYDLSQIOLICN---VTQGLSDIAVKNNGSVI 267
 Oy 51 KDGLPGIGGHHYSLHEYSVWKANLSEVYSSVLCVANTSTREYV-GAFQTSIONI-SFSGF 108
 Db 268 DEDDPVYLGEDYSEVEN---PANKRRSPFLIVLNLISIESRPFKHPFTGFANHTGIDAA 323
 Oy 109 TLRAGTGS---HYAAVLASLIVLALLAALLYVCRNLVLYWQD---YGVSEIND 161
 Db 324 YILQILPVNPFQKMHGICVLYIV--IVCSVFYIKFKIDILYWRDSCYFELPKSD 381
 Oy 162 GKLYDYAVSY-----SDCPEDKRFVNFILKPOLERGRGKFLFLDRDLLPAEPSA 212
 Db 382 GKTYDAIILPRKTVGEGSTDDC--IFERKVLPEVLEKCGKFLFYGRDYGEDIVE 438
 Oy 213 DLIVNLSCRRLLIVLSDAFSLRAMCShSREGICR-----LLEF-----TR 254
 Db 439 VINEENKRSRRLIILVRETSGFSLGSSSEQIAMYNALYODGIVKVLLELEKIDQYER 498
 Oy 255 RPIFTFEQGRDPAHPALRHLRQHRLLVTLML---RPGSVTPSSDQWKEVQLALP 308
 Db 499 MPISIKFIKOK---HGAIR-----WSGDFTQGPQSAKTRFPMKNVRYHMP 539
 RESULT 3
 G02426
 Interleukin-1 receptor-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
 C:Accession: G02426
 R:Loveberg, T.W.; Crowe, P.D.; Liu, C.; Chalmers, D.T.; Liu, X.
 Submitted to the EMBL Data Library, February 1996
 A:Reference number: H01239
 A:Accession: G02426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-562 <LOV>
 A:Cross-references: EMBL:U49065; NID:91236078; PIDN:AA853237.1; PID:91236079
 C:Superfamily: Interleukin-1 receptor type I
 Query Match 9.5%; Score 204; DB 2; Length 562;
 Best Local Similarity 28.5%; Pred. No. 4.3e-09;

Matches 81; Conservative 45; Mismatches 110; Indels 48; Gaps 15;

```
Oy      57 GIGHYSLHEYSWMKANLSEVLVSSVLGNVNTSPY-----YG-AFTCSIONISFSSFTLLQ 111
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     283 GVETHVSFRHH-----NLTYNITFELEVKMEDGLPFMCH-AGVSTAILIILQ 328

Oy     112 RAGTSHVAVALSLIVLALLAL-LYXACRNIVLMODAAGEVE-INDDKIDAVY 169
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    329 LPADPR-ALITGCLIALVAVASVYIYNIFKIDIIYMTMSAHSHTETLYDCKLTDAIV 387

Oy     170 SYSCPEPDKR-----FYVFILKPOLERRRGYKFLFDLRDLIPRAEPSADLVNLSR 220
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   388 LY---PPPHESORHAVDALVNILPIEVLERCCKKLTEGRDEPFOAAVANIDEVNYL 444

Oy    221 CRLIIVLSDAPLSRAMCShSFREGIC--RLLETTRRPITFPEGORDPAHP-ALRIUL 276
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   445 CRLTIIVVESIGFGLKNLSEEOIAVYSAIDOGMKVILILEKEIDETYVMPESIQYT 504

Oy    277 QRHRHLVTLLMRPGSVTPSSD----FWKEVOLALPKRYRYP 315
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   505 KKHGAIR--WH-GDETQSOCMKTKFKWKYVRHMPPR-RCPR 543

RESULT 4
A32604
Interleukin-1 receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 29-Sep-1999
C:Accession: A32604
R:Sims, J.E.; March, C.J.; Cosman, D.; Widmer, M.B.; MacDonald, H.R.; McMahon, C.J.; S.K.
Science 241, 585-589, 1988
A:title: cDNA expression cloning of the IL-1 receptor, a member of the immunoglobulin
A:Reference number: A32604; MUID:88290679
A:Accession: A32604
A:Molecule type: mRNA
A:Residues: 1-576<SIM>-
A:Cross-references: GB:M20658; GB:M29752; NID:g198300; PID:NAAA39279.1; PID:g309399
C:Superfamily: Interleukin-1 receptor type I
C:Keywords: cytokine receptor; glycoprotein; phosphoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-376/Product: Interleukin-1 receptor #status predicted <INT>
F:39-359/Domain: transmembrane #status predicted <TM>
F:46-99,145-199,251-315/Disulfide bonds: #status predicted
F:63,103,174,236,252,300/Binding site: carbohydrate (Asn) (covalent) #status pred
```

Query Match 8.9%; Score 190.5; DB 2; Length 576;
Best Local Similarity 24.0%; Pred. No. 6e-08;
Matches 86; Conservative 71; Mismatches 151; Indels 51; Gaps 18;

```
Oy      6 DRADPLSPEDDYLPALPAGSSVALNCTAMVVGSGHCSLPVOVLKKGFLGIGHYSTH 65
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    227 DR-PVLIISP-RNETIADGSGMIOLICH--VTGGFSDL-VYKRWNGSIEIMNDPFLAE 279

Oy     66 EYSWVK--ANLSEVLVSSVLGNVNTSEYWG-AFTCSIONIS-FSPTLQRAQPTSHVA 121
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   280 DYGVESHPSKKRYTLITLTINISEVKSQFYRRPFICYAKNKTNIPESAHVQLIYVPDPFN 339

Oy    122 VLASLAVL--ALLAALLAYKCRNLVLMODA---GGEINIDKLYRAYV----- 169
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   340 YLIGGFITLATIATVCVCATIKYKFQDIYLMWRDCSGFLPSKASDGKTAYAIYLKYKLG 399

Oy    170 ---SYSDCEPDERKVVNIILKPOLERRRGYKFLFDLRDLIPRAEPSADLVNLSRCRLIIV 227
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   400 EGNSDLD--TFEKALPEVLEEGGKFLPYGRDVGEDGTLEVTVNNVSKSRLLITI 456

Oy    228 LSDAFSLRAWCHSFPREGICRLLELTRRPITFP---EGQRDPAPHALRLLRHRLY 283
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   457 LVRDMGFGSLWGSSEQIATAYNALIOGKIIVLELEKIIDODEKMDSIQFIKO-KHEV 515

Oy    284 TLLIW-----RFGSVTPSSDFWKEVOLALPKRYR-----YRVPEGDPOTLODDKPM 331
       1 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   516 --IOWSDPEDPERQSN--KTRFMKNILRYOMQAORSPLSKIRLLITLD----VDTKEKL 567
```


RESULT 5

S29498 lymphocyte antigen Ly84 precursor - mouse

N:Alternate names: 38.5K T1 glycoprotein; ST2L protein

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000

C:Accession: S29498; A33541; S17657; S07054

R:Yamagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tomioka, S.
FEBS Lett. 318, 83-87, 1993

A>Title: Presence of a novel primary response gene ST2L, encoding a product highly similar

A:Reference number: S29498; MUID:93170492

A:Accession: S29498

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-567 <TAN>

A:Cross-references: EMBL:D13695; NID:g286100; PIDN:BAA02854.1; PID:g286101

R:Lenz, R.; Hoffmann, S.; Wernskold, A.K.
Pfl. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989

A>Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to

A:Reference number: A33541; MUID:89345536

A:Accession: A33541

A:Molecule type: mRNA

A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <KLE>

A:Cross-references: GB:M24843; NID:g201103; PIDN:AAA0160.1; PID:g201104

R:Tominaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
Biochim. Biophys. Acta 1090, 1-8, 1991

A>Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal map

A:Reference number: S17657; MUID:91355215

A:Accession: S17657

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <TKO>

A:Cross-references: EMBL:X60184; NID:g54200; PIDN:CAA42742.1; PID:g54201

R:Tominaga, S.I.
FEBS Lett. 258, 301-304, 1989

A>Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si

A:Reference number: S07054; MUID:90092495

A:Accession: S07054

A:Molecule type: mRNA

A:Residues: 1-328, 'SKECPSHIA' <TQ2>

A:Cross-references: EMBL:X07519; NID:g55517; PIDN:CAA68812.1; PID:g55518

A>Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator

C:Genetics:

A:Gene: ST2

A:Position: 1

A:Exons: 27/1, 97/2, 155/3, 210/1, 233/1, 280/2

C:Superfamily: Interleukin-1 receptor type I

C:Keywords: glycoprotein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-337/Product: ST2 protein #status predicted <MAT>

F:60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status

Query Match

Best Local Similarity 8.8%; Score 189.5; DB 2; Length 567;

Matches 82; Conservative 59; Mismatches 153; Indels 37; Gaps 14;

QY 9 PDLSPSEDQVLRPALGSSVALNCTAMVVGSPHSLPSYQWIKDKGLIGIGHYSLHEYS 68

DB 217 PVITNPNHNTMEVEIFGKPSIACSGKSH-FLADVLMOINKTIVGNFGARIQEEH 275

QY 69 WVKANLSEVL--VSSYLVG-VNTSTEV---YGAFTCSIONISSTLTORAGTSH--VA 120

DB 276 GRNESSNDMDCTSVLRGTGVEKDSLSEYDCLALNLHGMIKRTIRLRKQPIDHRSY 335

QY 121 AVLASLVLLALLALLVK-C-RLNVLWYODAYGEVEI-NDGKLYDAVVS----- 171

DB 336 YIVAGSLLMFINVLYLVKFWIEVALFWRDIVPYTRNDGKIXDAIYIPRFGRS 395

QY 172 -SDCPEDRKVFNFILKPOLERRRGYKLLDRLDLPRAEPSADLVNLSRCRLIYVLS 230

DB 396 AAGTHSVEYFVHTLPDVLNKGKGYKLCIXGRDLLPGQAAAFVSSIONSRQVFLAP 455

RESULT 6

JQ1526 Interleukin-1 receptor I precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 29-Sep-1999

C:Accession: JQ1526

R:Guida, S.; Heguy, A.; Mell, M.
Gene 111, 239-243, 1992

A>Title: The chicken IL-1 receptor: differential evolution of the cytoplasmic and ext

A:Reference number: JQ1526; MUID:92175529

A:Accession: JQ1526

A:Molecule type: mRNA

A:Residues: 1-555 <GVU>

A:Cross-references: GB:M81846; NID:g212206; PIDN:AAA48924.1; PID:g212207

A:Experimental source: embryo

C:Superfamily: Interleukin-1 receptor type I

C:Keywords: cytokine receptor; transmembrane protein

F:1-13/Domain: signal sequence #status predicted <SIG>

F:20-555/Product: Interleukin-1 receptor I #status predicted <INT>

F:339-359/Domain: transmembrane #status predicted <TRA>

Query Match

Best Local Similarity 8.6%; Score 184; DB 2; Length 555;

Matches 90; Conservative 65; Mismatches 101; Indels 104; Gaps 21;

QY 9 PDLSPSEDQVLRPALGSSVALNCTAMVVGSPHSLPSYQWIKDKGLIGIGHYSLHEYS 52

DB 230 PERTYRN-NNTIEVLGSHVMECN--VSSGYGLLPYQVNDVEDSDTYRDFEYEE 286

QY 53 GLPLIGIGHYSLHEYSWVKANLSEVLSSVLYGVNTSTEVYGAFTCSI-ONISFSTLQ 111

DB 287 GMPHGIA-----VSGTFENISEVLKDY-----AYKFCFIYDSQEFSTY-IR 329

QY 112 RAGPTSHVAVL-----ASLLVLLALLLVKCKLANLWQDXYGEV---EINDGKL 164

DB 330 LEHPVONIRGYLIGGISLIFLFLIL--IVYKIFIDIVLWYRSSCHPLGKKVSDGKI 387

QY 165 YDAYVYSDCPEDRK-----FVNFILKPOLERRRGYKLLDRLDLPRAEPSADL- 215

DB 388 YDAVLYX---PKNRSECLYSSDIFALKILPEVLERQCGYNLFIQGNL-AGEAVYDVID 443

QY 216 VNLSCRRLIVL-----SDAFLSRWCSHSPREG-CLLELTR-----R 255

DB 444 EKIHQSRVYIILVPEPCGYLIEDASEKHL--AVYNALIQDGIKILILEKIEDYANM 501

QY 256 PIPTFEGORRDPANHALLL-----RQHRHLVTLMLMRPGSTPSDWEKVEQLAPRK 310

DB 502 PESIKYVKOK---YGAIRWTGDFSERH-----SASTRWKVRVRYHMPSR 543

RESULT 7

A29943 Toll protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 02-Jun-2000

C:Accession: A29943

R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988

A>Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity,

A:Reference number: A29943; MUID:88135760

A:Accession: A29943

A:Molecule type: DNA

A:Residues: 1-1097 <HAS>

A:Cross-references: GB:M19969; GB:J02682; NID:g158640; PIDN:AAA26941.1; PID:g158641
 C:Genetics:
 A:Gene: FlyBase:Fl
 A:Cross-references: FlyBase:FBgn0003717
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
 C:Keywords: transmembrane protein
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-1097/Product: toll protein #status predicted <MAT>

Query Match
 Best Local Similarity 8.2%; Score 176; DB 2; Length 1097;
 Matches 70; Conservative 47; Mismatches 89; Indels 66; Gaps 13;

OY 121 AVIALTLVALLALLALLV-----VKGR-----NVLLMTQDAVGEVINDGLYDAVYSYS 172
 DB 810 AVIALTLVALLALLALLV-----VKGR-----NVLLMTQDAVGEVINDGLYDAVYSYS 172
 OY 173 DCEDEKRFVNFILKPOLER-RRGYFLFLDDNDLLPRAEPAADLVNLSRCRLIVLSDA 231
 DB 867 H--KDSFIEDLVLPQLEHGPOKQFQDLYEHNDMLVGHIPENIMRSVADSRRITVLSQN 924
 OY 232 FLIRACMSHSFR-----EGLCRLELTTRPIFTFEQGRDPAHPALRLRHRHLY 283
 DB 925 FLIRACMSHSFR-----EGLCRLELTTRPIFTFEQGRDPAHPALRLRHRHLY 283
 OY 284 TLLWRPQSVPPSSD--FKREVOLALPRKVRPVEGDPQOTLODDKPMILRGVPEG 341
 DB 976 TYLKW-----GDPWMDKRLRFLPR--RV-----GNIGNG 1005
 OY 342 RALDSEVDPDEGDLGVGKGVGPRSPAPPHTS 373
 DB 1006 ALIKTALKGSTDDKLELKP---SPVTPPLTF 1034

RESULT 8
 156526
 Interleukin 1 receptor type I - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 29-Sep-1999
 C:Accession: 156526
 R:Heart, R.P.; Liu, C.; Shadick, A.M.; McCormack, R.J.; Jonakait, G.M.
 J:Neuroimmunol. 44, 49-56, 1993
 A:Title: An mRNA homologous to interleukin-1 receptor type I is expressed in cultured rat
 A:Reference number: 156526; MUID:93266794
 A:Accession: 156526
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-390 <RES>
 A:Cross-references: GB:M95578; NID:g451305; PIDN:AAA16196.1; PID:g451306
 C:Superfamily: interleukin-1 receptor type I
 C:Keywords: cytokine receptor

Query Match
 Best Local Similarity 7.8%; Score 168.5; DB 2; Length 590;
 Matches 88; Conservative 56; Mismatches 128; Indels 83; Gaps 21;
 OY 6 DPAPPLSPSEDOVLRPALGSSVLANCTANVSGPHGSLSPYOMLDCPLIGIGHYSUH 65
 DB 241 DR-PVIMSP-RNEMTEADPGSTIOLCN--VIGQFIDL--VYMKNGSEIEMDDPIAE 293
 OY 66 EYSWVK--ANLSELVSVYGVNVTSEYVG-AFTCSIONISFSFTIORAGPTSHVAA 121
 DB 294 DQFLEHPSARRYTLIT--LNVSEVSKOYRYPFCVKNHILE-----TAHVRL 344
 OY 122 VLA-----SLVLLALLLALLVYC-----RLNVLYADAYGEV--EINDGLYDA 167
 DB 345 VYVPDPRKNVILGFAIFTAVFCACIKVFKVDIVLWYRSCSDFLPKRASDGRYDA 404
 OY 168 YVSSDCPEDRKRV--NFLK--PO-LERRGYKFLDDRLRLRAPASADLVNLSRC 221
 DB 405 YLVPKTYGSGSAVYLDTFVFKLLPEVLEGGQYKFLICGNDYVGEPTIEVTENKRS 464
 OY 222 RLRLVLSDAFLSRWCSHS-----FREGI-CRLLEL-----TRRPIFTFEG 263

DB 465 RRLIITLVDMKSFSCLOQSSFEQIAITDALIRGIIKILILEKIDYKMPESIOFIK 524
 OY 264 QRRDPAPRLRLRLRHRHLVTLILM-----RPSVPSDDFWKEVOLAPRKVR 312
 DB 525 QK-----HGA-----ICNSGDFKRFQSA--KTRFWKNRLRYQMPAQR 560

RESULT 9
 542633
 Fil-1M protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2000
 C:Accession: 542633
 R:Bergers, G.; Reikertorfer, A.; Braselmann, S.; Graninger, P.; Busslinger, M.
 A:Title: Alternative promoter usage of the Fos-responsive gene Fil-1 generates mRNA 1
 A:Reference number: 542632; MUID:94178260
 A:Accession: 542633
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-247 <BER>
 C:Superfamily: Interleukin-1 receptor type I

Query Match
 Best Local Similarity 7.6%; Score 163; DB 2; Length 247;
 Matches 65; Conservative 39; Mismatches 95; Indels 32; Gaps 11;

OY 110 LORAGPTSHVAA--VLASLVALLALLVYC--RLNVLYADAYGEVINDGLY 165
 DB 3 LRRKOPIDHOSYTYVAGCSLLMFINVLYLVKVFIEVALRMDMADYKQNDGKLY 62
 OY 166 DAVSY-----SDCEDKRFVNFILKPOLERRRGYKFLDDRLRLPRAEPAADLVN 217
 DB 63 DAVIYTPRVFNGSAGCTSVFVHYTLPOYLENKGCKYKQIIGRDLQDAVYESS 122
 OY 218 LSRCLRLIVLSDAPLIRACMSHSFRGL-CRLLELRRIEFTFEQGRDPAHPALRL- 275
 DB 123 IONSRYQFVLAIPHMHSEKFAEQEIALSHALIONNSKYLILEM-----FGEASRLQ 177
 OY 276 ---LRQH-RHLVTL--LIMRPGSVTP-----SSDFWEVOLAPRKVRYP 315
 DB 178 LGDLDLSLQHLVKMGQTIKWNEDHVDKOSLSKFWKHVRYPMP--VPRKP 226

RESULT 10
 713887
 Fil protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C:Accession: 713887
 R:Chiang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A:Title: Expression of a novel Toll-1-like gene spans the parasegment boundary and controls
 A:Reference number: 713887; MUID:95151581
 A:Accession: 713887
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1385 <CHI>
 A:Cross-references: EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAA33383.1
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0004364
 A>Note: Fil

Query Match
 Best Local Similarity 6.7%; Score 144.5; DB 2; Length 1385;
 Matches 68; Conservative 44; Mismatches 104; Indels 45; Gaps 12;
 OY 99 STONTSFSSFLORAGPTSHVAAVLASLVALLALLVYC--RLNVLYADAYGEVINDGLY 155
 DB 979 SASNTSSQ---DLAG--GRLPLAVALVILFDVLLIVFVRESVAMLFVHGYVRA 1033
 OY 156 EVELND-GKLYDAVYSIDCPEDKRFVNFILKPOLER-RRGYKFLDDRLRLPRAEPA 212

```
Db 1034 CEPREFDAGLTYDAIILHSE--KDYEFCVCRNIAEILEHGHPRPRLTIOQRDLPPQAS-HL 1090
QY 213 DILVINSRCRLIVLSDAFLSRAMCShSFRELCRLLE-LTRRRPIFI---TTEGQRDP 268
Db 1091 QLVGARASRKIIIVLTRNLALATEMNRIEFRNAFHESLRGLAOKLVIIEETSVSAEAEDV 1150
QY 269 AH-----PALRLRQHRHLVTLMLRPGSVTPSSDFKREVOALPRKV--RYRVEG 318
Db 1151 AELSPYLKSPSRNRLTCDRY-----FWEKLRVAILPILSRGNNTYL 1193
QY 319 DPQTOLODDKDPMLILGRVP 339
Db 1194 DHHERFKOPVSPGMIFRQAPR 1214

RESULT 11
11.2
Q: wheeler protein - fruit fly (Drosophila melanogaster)
C: Species: Drosophila melanogaster
C: Date: 20-Sep-1999 #sequence: revision 20-Sep-1999 #text_change 17-Nov-2000
C: Accession: T13852
R: Elidon, E.; Kooyer, S.; D'aveylyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Belien, H.
Development 120, 885-899, 1994
A: Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A: Reference number: 217796; PMID:95324375
A: Accession: T13852
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-1389 <EID>
A: Cross-references: EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAAT9208.1
C: Genetics:
A: Gene: wheeler
A: Cross-references: FlyBase:FBgn0004364

Query Match 6.5%; Score 139.5; DB 2; Length 1389;
Best Local Similarity 23.2%; Pred. No. 0.0036;
Matches 66; Conservative 51; Mismatches 105; Indels 63; Gaps 12;

QY 75 SELVSSVGLVANTSTEVYCAFCSTIONISFSSFTLQRAQPSHVAVALSLVLLALL 134
Db 973 SDLLDASASNIS--SSODLACAIIC-----PCWPAVLVILFLVV 1009
QY 135 AALLVYKCRNLVLMYQDAG----EVEIND-GKLYDAVSYSDCPEDRKFVETLKPOL 189
Db 1010 VLLIVFVRSVAMMLPAHKGVAVCEPRFEDAGKLDIAIILHSE--KDYEFCVCRNIAEL 1067
QY 190 ER-RRGYKFLDRLDRLPRAEPSADLLVNLSCRLIVLSDAFLSRAMCShSFREGICLR 248
Db 1068 EHGRPPFRLCIGQRDLPPQAS-HLQLVGARASRKIIIVLTRNLALATEMNRIEFRNAFHE 1126
QY 249 LLE-LTRRRPIFI---TTEGQRDPAH-----PALRLRQHRHLVTLMLRPGSVTPS 296
Db 1127 SLGGLQAKVLIETSTVSAAEVAELSPYLKSPSRNRLTCDRY-----FWEKLRVAILPILSRGNNTYL 1171
QY 297 SDFWKEVOLALPRKV--RYRVEGDPOTOLDDKDPMLILGRVP 339
Db 1172 --FWEKLRVAILPILSRGNNTYL DHHERFKOPVSPGMIFRQAPR 1214

RESULT 12
12.1
type 1 interleukin-1 receptor - rat (fragment)
C: Species: Rattus sp. (rat)
C: Date: 12-Aug-1996 #sequence: revision 12-Aug-1996 #text_change 13-Sep-1998
C: Accession: I51903
R: Sutherland, D.B.; Varilek, G.W.; Neill, G.A.
Am. J. Physiol. 266, C1198-C1203, 1994
A: Title: Identification and characterization of the rat intestinal epithelial cell (IEC-
A: Reference number: I51903; PMID:94262728
A: Accession: I51903
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
```

```
A: Residues: 1-169 <RES>
A: Cross-references: GB:S70238; NID:g546976
A: Experimental source: intestinal epithelial IEC-18 cells
C: Superfamily: interleukin-1 receptor type I
C: Keywords: cytokine receptor

Query Match 6.0%; Score 128.5; DB 2; Length 169;
Best Local Similarity 28.1%; Pred. No. 0.002;
Matches 50; Conservative 29; Mismatches 76; Indels 23; Gaps 6;

QY 145 NVLLMYQDAYGEV---EINDGKLYDAYVSYSDCPEDRKFV---NFTLK--PQ-LERRRY 195
Db 1 DIYLMYRDSCDPLPPKASDQKTYDAYVLYPKYGGSPAYLDTFVFKLLPEVLEGGQFGY 60
QY 196 KFLPDRDLPRAPESADLLVNLSCRLIVLSDAFLSRAMCShSFREGICRLLETTR 255
Db 61 KLFICGRDYYVGEPTLEVTEWENKRSRRLIILVRDMGFSFCGSGSEQOIAIYALIRE 120
QY 256 PIRTF---EGQRDPAPHALRLRQHRHLVTLMLRPGSVTPSSDFKREVOALPR 309
Db 121 GIKIILLELEIODYEKMEPSIOFIKQ-----KHGATCGSDFKERPOSATKR 168

RESULT 13
S18209
fibroblast growth factor receptor 4 precursor (clone 61) - mouse
N: Alternate names: tyrosine kinase Mpk-11
N: Contains: protein-tyrosine kinase (EC 2.7.1.112)
C: Species: Mus musculus (house mouse)
C: Date: 07-Oct-1994 #sequence: revision 07-Oct-1994 #text_change 16-Jul-1999
C: Accession: S18209; S26751; S30497
R: Stark, K.L.; McMahon, J.A.; McMahon, A.P.
Development 113, 641-651, 1991
A: Title: FGFR-4, a new member of the fibroblast growth factor receptor family, expres
A: Reference number: S18209; PMID:92146274
A: Accession: S18209
A: Molecule type: mRNA
A: Residues: 1-799 <STAI>
A: Cross-references: EMBL:X59927
R: Stark, K.L.
submitted to the EMBL Data Library, May 1991
A: Reference number: S26751
A: Accession: S26751
A: Molecule type: mRNA
A: Residues: 1-485, 'QVYRAEAFG', 486-799 <STA2>
A: Cross-references: EMBL:X59927; NID:g50968; PIDN:CAA42551.1; PID:g50969
R: Giaraldi-Hedensstrelt, P.; Nieto, M.A.; Fraint, M.; Mattei, M.G.; Chestier, A.; Wilkin
Oncogene 7, 2499-2506, 1992
A: Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed i
A: Reference number: S30496; PMID:93096484
A: Accession: S30497
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 611-667 <GIL>
A: Cross-references: EMBL:X57236; NID:g53187; PIDN:CAA40512.1; PID:g53188
C: Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr
C: Keywords: ATP; duplication; glycoprotein; growth factor receptor; phosphotransferas
F: 19-799/Product: fibroblast growth factor receptor 4 #status predicted <STO>
F: 19-366/Domain: extracellular #status predicted <EXT>
F: 162-223/Domain: immunoglobulin homology <IMM>
F: 367-387/Domain: transmembrane #status predicted <TM>
F: 388-799/Domain: intracellular #status predicted <INT>
F: 462-747/Domain: protein kinase homology <KIN>
F: 470-478/Region: protein kinase ATP-binding motif
F: 54-98, 169-221, 268-330/Disulfide bonds: #status predicted
F: 500, 517, 609/Active site: Lys, Glu, Asp #status predicted

Query Match 5.7%; Score 123; DB 2; Length 799;
Best Local Similarity 22.1%; Pred. No. 0.043;
Matches 103; Conservative 45; Mismatches 136; Indels 182; Gaps 23;

QY 24 LGSSVALNCTAWVSPGHCSLPSVQWLK----DGLPLGIGGHSLSHEYSMVKNANSEVLV 79
```

```

Db 260 VGSDFVLLCKVYSDADPH-----IOMLKHYVINGSSFGADGFPYQVLTPTDINISEV-- 312
OY 80 SSVLYGVNVTSTEVYGAFTCSION---ISFSS-----FTLORAGP-----TSHVAV 122
Db 313 -QVLYLRNVSADGAGETCTAGNSIGLSYQSAWLYLVEEDLTMTATPEARTDIIILYV 371
OY 123 LASLLVLLALLLAAIIVKCRNLVLLWYODAYGEVEINDKLYDAYVSYDCPEDRKFEVN 182
Db 372 SGGSLVLLVLLLVAGYVHROY-----IRGHYSROPVTIOKL-----SRPLAKRF-- 415
OY 183 FIIRKPLEER-----RGYKFLDDRDLIPRAEPSADLLVNLRCRRLIIVLSDAF 232
Db 416 -----SLESRSSGKSSLSLVGRVRLSSGCPPLITG-----LVNL-----DLP 452
OY 233 LSRAMGSHSFREGICRLLELTR-----RPT-----FITTEGORRDPAPH----- 271
Db 453 LDDPLW-----EPPRDLVYLGKPLGEGCGQVYRAEAFQMDPSRPDQSTVAV 499
OY 272 -----ALRLRQHRHLYTLILMPRGSVTPSSDPFWKEVOLALPRKV 311
Db 500 KMLKDNASDKDLADLYSEMEVWKILGRNKNITNL---GVCTQHGPLYVIVECAKGNL 555
OY 312 RFRPVSGDPQTQLODDKDPMILIRGVPRGRALDSEVDPDPEDGCVKQPVFGEPSAPPH 371
Db 556 RE-----FLRARPPG-----PDLSPDGPPRSSGPL---SPPAL 586
OY 372 TS-----GVALGSRSSSEVDVSDLSGRNYSARKDFYCIYKSDM 410
Db 587 VSCAVGVARGMQYLESR--KCIHRDLAARN-----VLYTEDV 622

```

RESULT 14

```

S11226
MyD88 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S11226; J02079
R:Lord, K.A.; Hoffman-Liebermann, B.; Liebermann, D.A.
Oncogene 5, 1095-1097, 1990
A:Title: Nucleotide sequence and expression of a cDNA encoding MyD88, a novel myeloid di
A:Reference number: S11226; MUID:90326414
A:Accession: S11226
A:Molecule type: mRNA
A:Residues: 1-243 <LOR>
A:Cross-references: EMBL:X51397; NID:953293; PIDN:CAA35762.1; PID:953294
R:Hultmark, D.
Biochem. Biophys. Res. Commun. 199, 144-146, 1994
A:Title: Macrophage differentiation marker MyD88 is a member of the TOLL/TL-1 receptor f
A:Reference number: J02079; MUID:94168566
A:Notes: annotation

```

Query Match 5.4%; Score 115; DB 2; Length 243;

Best Local Similarity 29.2%; Pred. No. 0.044;

Matches 33; Conservative 26; Mismatches 38; Indels 16; Gaps 5;

```

OY 163 KLYAYVYSDCPEDRKFEVNFILKPOLERRRGYKFLFDDRDLPRA--EPSADLVNLS 219
Db 106 ELFAFICY--CPNDIEVQEMIRQLQTDYRLKLCVSDRVLPGTCWVSIASELIE--K 161
OY 220 RCRRLIVLSDAFLSRAMGSHSFREGICRLLELT-----RRPIITTEGORRD 267
Db 162 RCRMVVVVSDYLSQSKCEDFOTKFA-----LSLSPGVQOKRLPIKYYKAMKD 210

```

RESULT 15

```

T08664
Toll protein-like receptor DKFp54710610.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C:Accession: T08664
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999

```

```

A:Reference number: 216466
A:Accession: T08664
A:Molecule type: mRNA
A:Residues: 1-786 <POU>
A:Cross-references: EMBL:AL050262
A:Experimental source: fetal brain; clone DKFp54710610
A:Note: DKFp54710610.1

```

Query Match

Best Local Similarity 22.8%; Score 114.5; DB 2; Length 786;

Matches 49; Conservative 39; Mismatches 88; Indels 39; Gaps 9;

```

OY 119 VAAVLASLVLLALLLAAIIVKCRNLVLLWYODAYGE-----VEINDKLY 165
Db 583 IVTLVATMLVLAIVTSLCITYLD-----LPWYLRWVCOWTQTRRRARANIPLERLQNLQF 637
OY 166 DAYVSYDCPEDRKFEVNFILKPOLERRRGYKFLFDDRDLPRAEPSADLLVNLRCRRLI 225
Db 638 HAFISYSG--HDSFWVKNELLPNLE--KEGMOICLHERNFVPGKSIVENIITCIKSKYSL 694
OY 226 VVLSDAFLSRAMGSHS-----FREGICRLLELTRRPIITTEGORRDPAHPALRL 276
Db 695 FVLSPNFVQSEWCHYELFYAHNMILFHGSSNLTILILEPI-----PQYSIPSSHYKLSL 749
OY 277 ROHRHLYTLILMPRGSVTPSSDPFWKEVOLALPRKV 311
Db 750 MARR--TYLEW--PKRSKRGLFWANLRAAINIKL 780

```

Search completed: November 7, 2002, 18:52:57
Job time : 49 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:47:01 ; Search time 1676 Seconds
(without alignments)
9929.442 Million cell updates/sec

Title: US-09-598-443-1
1333
Perfect score: 1 atgcacgagctgtctgtagatag.....tgccaagatgatagtag 1233
Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Seed: 13736207 segs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estb1a:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	733	59.4	763	10	BI517905 603041985
2	725.2	58.8	941	10	BG740350 602634105
3	681.4	55.3	821	10	BE797163 601587171
4	660.4	53.6	852	10	BI521062 603081652
5	639.2	51.8	749	10	BI821947 603039758
6	616	50.0	808	10	BI769076 603057053
7	606.6	49.2	791	10	BI518182 603041985
8	556.8	47.8	845	10	BE792803 601584677
9	556.8	45.2	941	10	BI518544 603061669
10	546.8	44.3	1067	10	BI752545 603021956
11	541	43.9	983	10	BI759065 603042860
12	535.8	43.5	796	10	BG742077 602633540
13	522.4	42.4	801	10	BI770099 603053464
14	513	41.6	783	10	BI820133 603037143
15	496.4	40.3	821	10	BI758455 603022612
16	488.4	39.6	513	10	BF239133 601905529
17	486	39.4	925	10	BI905958 603062841

18	482.2	39.1	970	10	BE250059 600943075
19	468.8	38.0	822	10	BI909088 603070070
20	467.8	37.9	892	10	BE612529 601452037
21	454.8	36.9	458	9	AV655410
22	452	36.7	463	10	BE304820 601143635
23	452	36.7	878	10	BI103498 60110498
24	446	36.2	627	10	BE279363 601157924
25	435	35.3	540	9	AW786417 119555 MA
26	434.4	35.2	773	10	BI837418 603086710
27	427.6	34.7	1021	10	BI519672 603061669
28	418.8	34.0	705	10	BE869865 601445507
29	411	33.3	565	9	BE293826 601186875
30	402	32.6	567	9	AW250249 2821373.5
31	399.2	32.4	536	10	BG609794 323769 MA
32	390	31.6	714	10	BI101849 602885412
33	377.2	30.6	410	9	AA310938 EST181714
34	366	29.7	822	10	BE869379 601445316
35	364.8	29.6	822	10	BI838735 603082175
36	357.4	29.0	720	10	BF971860 602240449
37	353.4	28.7	629	10	BG333328 602431365
38	350.6	28.4	863	10	BE293423 600943075
39	343.8	27.9	698	10	BI081911 602877135
40	343.8	27.9	723	10	BG971566 602840616
41	333	27.0	507	10	BE907720 601497752
42	331.8	26.9	650	9	AI451851 mx19h09.y
43	327.6	26.6	530	9	AI597102 m171f07.y
44	327.2	26.5	585	10	BG894625 355310 MA
45	318.6	25.8	1916	10	BF785809 602112433

ALIGNMENTS

RESULT 1
BI517905
LOCUS 603041985F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182556 5',
DEFINITION mRNA sequence.
ACCESSION BI517905
VERSION BI517905.1 GI:15342697
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 763)
NIH-MGC http://mgc.ncl.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11435 row: 1 column: 21
High quality sequence stop: 739.
Location/Qualifiers
1. 763
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182556"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 3 colons; age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is

FEATURES

source

QY 950 AAGAGACCCCGACGACGCTGC-AGGACGACAAGACCCCATGCTGATCTTTCGAGGC 1008
|||||
DB 541 AAGAGACCCCGACGACGCTGC-CAAGACGACGACGACCCCATCTGATCTTTCGAGGC 600
QY 1009 CGAGTCCCTGAGGCGGCGCCCTGG-ACTCAGAGGTGAGACCCCGGACCTGAGGCGGACT 1067
|||||
DB 601 CGAGTCCCTGAGGCGGCGCCCTGG-AGACTCAGAGGTGAGACCCCGGACCTGAGGCGGACT 660
QY 1068 GAGTGTCCGGGGGCGCTGTTTTGGAGAGCCATCAGCTCCACCGGACAGAGTGGGGCTTC 1127
|||||
DB 661 GGGTGTCCGGGGGCGCTGTTTTGGAGAGCCATCAGCTCCACCGGACAGTGGGGCTTC 720
QY 1128 GCTGGG-AGAGAGCCGAGCA--GCGAAGTGAGCTCTCGATCTCGGCTCGCGAAGCTA 1184
|||||
DB 721 GCTGGGAAGAGAGCCGGAAGCAAGCAAGTGAGCTCTCGATCTCGGCTCGCGAAGCTA 780
QY 1185 CAGTCCCGGACCA-GACTTCTACTGCTT-GGTGTCCAGGATGA 1226
|||||
DB 781 CAGTCCCGGACCAAGCTTCTACTGCTCGGAGTGTCCAGGATGA 824

RESULT 3
BE797163 821 bp mRNA linear EST 20-SEP-2000
LOCUS 60158717f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941561 5',
DEFINITION mRNA sequence.
ACCESSION BE797163
VERSION BE797163.1 GI:10218361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 821)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCPD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LCM793 row: m column: 18
High quality sequence stop: 793.
Location/Qualifiers
1..821
F.ES
Source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3941561"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site: 1; XhoI; Site: 2;
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 141 a 270 c 250 g 160 t
ORIGIN

Query Match 55.3%; Score 681.4; DB 10; Length 821;
Best Local Similarity 94.4%; Pred. No. 9.9e-112;
Matches 728; Conservative 0; Mismatches 41; Indels 2; Gaps 2;
QY 206 GGGTCAGGCGCAACCTGTCAAGAGTGTGTCCA-GTGTCTGGGGGTCAACCTGACC 264
|||||

DB 14 GGGTCAGGCGCAA-CTGTCAAGAGTGTGTGTCCATGTGTCTGGGGGTCAACCTGACC 72
QY 265 AGCACTGAAGTCTATGGGGCGCTTCACTGCTCCATCCAGAACATCAGGTTCCCTCCCTTC 324
|||||
DB 73 AGCACTGAAGTCTATGGGGCGCTTCACTGCTCCATCCAGAACATCAGGTTCTCTCTTC 132
QY 325 ACTCTTCAGAGAGCTGAGCCCTACAGACGAGTGGCTGGCTGGCTGGCTCCCTCCCTGCTC 384
|||||
DB 133 ACTCTTCAGAGAGCTGAGCCCTACAGACGAGTGGCTGGCTGGCTGGCTCCCTCCCTGCTC 192
QY 385 CTGCTGGCCCTGCTGCTGGCCGCTGCTCTATGTCAAGTCCGCTCAACGTGCTGCTC 444
|||||
DB 193 CTGCTGGCCCTGCTGCTGGCCGCTGCTCTATGTCAAGTCCGCTCAACGTGCTGCTC 252
QY 445 TGGTACCAAGAGCGGTATGGGAGGTGGAGATTAACGAGCGGAACCTCTACAGCCCTAC 504
|||||
DB 253 TGGTACCAAGAGCGGTATGGGAGGTGGAGATTAACGAGCGGAACCTCTACAGCCCTAC 312
QY 505 GTCTCTCAAGAGAGCTGCGCGAGAGCCGCAAGTTCGTAACCTTCATCTTAAGCCGAG 564
|||||
DB 313 GTCTCTCAAGAGAGCTGCGCGAGAGCCGCAAGTTCGTAACCTTCATCTTAAGCCGAG 372
QY 565 CTGAGCGCGCTGCGGGCTTACAGCTTCTTCGAGCAGACCGGACCTCTGCGCGGCT 624
|||||
DB 373 CTGAGCGCGCTGCGGGCTTACAGCTTCTTCGAGCAGACCGGACCTCTGCGCGGCT 432
QY 625 GAGCCCTCGCGGACCTCTTGGTGAACCTGAAGCGGCTGCCAGCGCTCATGCTGCTGCT 684
|||||
DB 433 GAGCCCTCGCGGACCTCTTGGTGAACCTGAAGCGGCTGCCAGCGCTCATGCTGCTGCT 492
QY 685 TCGAGCGCGCTTCTGAGCGCGGCTGCTGAGCGACGACCTTCCGAGAGGCGCTGCGCG 744
|||||
DB 493 TCGAGCGCGCTTCTGAGCGCGGCTGCTGAGCGACGACCTTCCGAGAGGCGCTGCGCG 552
QY 745 CTGCTGAGCTACCCGCAAGACCATCTTTCATCATCTTCGAGAGCGCGAGCGGACCC 804
|||||
DB 553 CTGCTGAGCTACCCGCAAGACCATCTTTCATCATCTTCGAGAGCGCGAGCGGACCC 612
QY 805 GCGCACCGGCGCTCGGCTGCTGCGCAGACGCGGCACTGGTGAACCTGCTGCTGCG 864
|||||
DB 613 GCGCACCTGCGGCTCGGCTGCTGCGCAGACGCGGCACTGGTGAACCTGCTGCTGCG 672
QY 865 AGGCCGCGGCTCGGCTGCTGCTGCTGCGGAAAGAGTGGACAGTGGCGTGGCG 924
|||||
DB 673 AGGCCGCGGCTGCTGCTGCTGCTGCTGCGGAAAGAGTGGACAGTGGCGTGGCG 732
QY 925 CGGAAGTTCGGTACAGGCGGTTGGAAGAGACCCCGAGCGAGCTGACG 975
|||||
DB 733 GGAAGTTCGGGAACAGGCGGTTGGAAGAGAACCCCAAGAGGCAATTGACG 783

RESULT 4
B1521062 852 bp mRNA linear EST 29-AUG-2001
LOCUS 603081652f1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220901 5',
DEFINITION mRNA sequence.
ACCESSION B1521062
VERSION B1521062.1 GI:15345854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 852)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LAM11555 row: 9 column: 14
 High quality sequence start: 3
 High quality sequence stop: 780.
 Location/Qualifiers

FEATURES

source

1..852
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5220901"
 /clone_1lb="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: Pooled pancreas and spleen; Vector: PCMV-SPOrt6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1.2-5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
 B...COUNT 138 a 284 c 255 g 175 t
 ORIGIN

Query Match 53.6%; Score 660.4; DB 10; Length 852;
 Best Local Similarity 98.7%; Pred. No. 5.4e-108;
 Matches 697; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

OY 1 ATGCGAGTGTCTGTGATAGGCGCCCTGACTCTCTCCCGTCGAGACAGAGTGTG 60
 Dn 148 ATGCGAGTGTCTGTGATAGGCGCCCTGACTCTCTCCCGTCGAGACAGAGTGTG 207

OY 61 AGGCGTGTGGGCGAGCTGAGTGGCTGGAACATGACAGGCTGGGATGATGCGGCC 120

Dn 208 AGGCGTGTGGGCGAGCTGAGTGGCTGGAACATGACAGGCTGGGATGATGCGGCC 267

OY 121 CACTGCTCCCTGCTTCAATCCAGTGGGCGAAGAGGCGCTTCCATTGGGAATGGGGCG 180

Dn 268 CACTGCTCCCTGCTTCAATCCAGTGGGCGAAGAGGCGCTTCCATTGGGAATGGGGCG 327

OY 181 CACTACAGCTCCAGAGTACTCTGGGTCAAGGCCAATCTGACAGAGTGTGTCTC 240

Dn 328 CACTACAGCTCCAGAGTACTCTGGGTCAAGGCCAATCTGACAGAGTGTGTCTC 387

OY 241 AGTGTCTGGGGGTCAAGCTGACAGCACTGAAGTCTATGGGGCTTCCATCTGCTCATC 300

Dn 388 AGTGTCTGGGGGTCAAGCTGACAGCACTGAAGTCTATGGGGCTTCCATCTGCTCATC 447

OY 301 CAGAATCATGAGTCT 360

Dn 448 CAGAATCATGAGTCT 507

OY 361 GGGGTCTGTGGGCT 420

Dn 508 GGGGTCTGTGGGCT 567

OY 421 AATGCTCTCTCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480

Dn 568 AATGCTCTCTCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 627

OY 481 GAGGGAAGCTCTACAGAGCT 540

Dn 628 GAGGGAAGCTCTACAGAGCT 687

OY 541 GTGAATTCATCTAAAGCCGAGCTGGA - GGGGGTGGGGGTCTAAAGTCTCTCTGGA 599

Dn 688 GTGAATTCATCTAAAGCCGAGCTGGA - GGGGGTGGGGGTCTAAAGTCTCTCTGGA 747

OY 600 CGACCGGAGCTCTGCGCGCGCTGAGCCCTCGCGGAGACTCTTGGGAACCTGGA - GCC 658

Dn 748 CGACCG - GACCTCTGCGCGCGCGCTGAGCCCTCGCGGAGACTCTTGGGAACCTGAGGCC 806

OY 659 GCTGCCGACGCTCTCATGCTGTGCTTTGGAGCGCTTCTGAGCCG 704
 Dn 807 GGTGCCGACGCTCTCATGCTGTGCTTTGGAGCGCTTCTGAGCCG 852

RESULT 5

BI821947

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 749)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LAM11450 row: d column: 16
 High quality sequence stop: 739.
 Location/Qualifiers

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 /note="Organ: Pooled brain, lung, testis; Vector: PCMV-SPOrt6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
 BASE COUNT 127 a 262 c 218 g 142 t
 ORIGIN

Query Match 51.8%; Score 639.2; DB 10; Length 749;
 Best Local Similarity 99.5%; Pred. No. 3.1e-104;
 Matches 641; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 203 CCTGGGTCAAGGCCAAGCTGTCAAGGTCTTGTGTCAAGTGTCTGAGGCTCAAGCTGA 262

Dn 106 CCTGGGTCAAGGCCAAGCTGTCAAGGTCTTGTGTCAAGTGTCTGAGGCTCAAGCTGA 165

OY 263 CCAGCACTGAAGTCTATGGGGCTTCAAGCTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGT 322

Dn 166 CCAGCACTGAAGTCTATGGGGCTTCAAGCTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGT 225

OY 323 TCACCTTTCAGAGAGTGTGGGCTTCAAGGCGAGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 382

Dn 226 TCACCTTTCAGAGAGTGTGGGCTTCAAGGCGAGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 285

OY 383 TCTGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 442

Dn 286 TCTGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 345

OY 443 TCTGTTACAGAGCGGCTATGGGAGGTGAGATTAAGCAGGGAAGCTCTACGAGCGCT 502

|||||
Db 346 TCTGTACACGACGGGTATGGGAGGTAGATAAAGACGGAGACTCTACGACGCT 405
OY 503 AGCTTCCTCCACAGCCAGCTCCCCGAGGACCGCAAGTTCGTGAACCTATCTTAACCCG 552
Db 406 AGCTTCCTCCACAGCCAGCTCCCCGAGGACCGCAAGTTCGTGAACCTATCTTAACCCG 465
OY 563 AGCTGAGGCGGCTCGGGGCTACAAAGCTCTCTCTGAGCAGCAGCAGCTCTCGCGCG 622
Db 466 AGCTGAGGCGGCTCGGGGCTACAAAGCTCTCTCTGAGCAGCAGCAGCTCTCGCGCG 525
OY 623 CTGAGCCCTCCGCGGACCTCTCTGAGTGAACCTGAGCCGCTGCGGACCTCATCTGTGTG 682
Db 526 CTGAGCCCTCCGCGGACCTCTCTGAGTGAACCTGAGCCGCTGCGGACCTCATCTGTGTG 585
OY 683 TTTCGAGGACCTCTCTGAGCAGCCGCGGCTGTGTGACGACCAAGCTTCGCGGAGGCTGTGCG 742
Db 586 TTTCGAGGACCTCTCTGAGCAGCCGCGGCTGTGTGACGACCAAGCTTCGCGGAGGCTGTGCG 645
OY 743 GGCTGTGAGCTACACCCGACAGCCATCTTCACTTCAGAGGCGCAGAGCGGACG 802
Db 646 GGCTGTGAGCTACACCCGACAGCTATCTTCACTTCAGAGGCGCAGAGCGGACG 705
OY 803 CCGCGACCCCGGCGCTCCGCTGCTGCGGACGACCGGACCTG 846
Db 706 CCGCGACCCCGGCGCTCCGCTGCTGCGGACGACCGGACCTG 749
RESULT 6 808 bp mRNA linear EST 25-SEP-2001
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DEFINITION mRNA sequence.
ACCESSION B1769076
VERSION B1769076.1 GI:15760654
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 808)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1517 row: 1 column: 13
High quality sequence stop: 807.
Location/Qualifiers
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/clone_11b="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 150 a 262 c 231 g 165 t

ORIGIN
Query Match 50.0%; Score 616; DB 10; Length 808;
Best Local Similarity 97.4%; Pred. No. 4, 2e-100;
Matches 637; Conservative 0; Mismatches 15; Indels 2; Gaps 1;
OY 4 CCAGGTGTCTGTGATAGGAGCCCTGACTTCCTCTCCGCTGGAAGACGAGTGTGAG 63
Db 155 CCAGGTGTCTGTGATAGGAGCCCTGACTTCCTCTCCGCTGGAAGACGAGTGTGAG 214
OY 64 CCGCTGAGGACGCTCACTGAGTGGCTGAACTGACGCGCTGGGTAGTCTCTGGGCCAC 123
Db 215 CCGCTGAGGACGCTCACTGAGTGGCTGAACTGACGCGCTGGGTAGTCTCTGGGCCAC 274
OY 124 TGTCTCCCTGCTTCACTCACTGAGTGGCTGAAAGAGGCGCTTCATTTGGGAATTTGGGGCCAC 183
Db 275 TGTCTCCCTGCTTCACTCACTGAGTGGCTGAAAGAGGCGCTTCATTTGGGAATTTGGGGCCAC 334
OY 184 TACAGCTCCACAGTACTCTGAGGCTCAAGGCGCAACCTGACAGAGTGTGTGCTGAGT 243
Db 335 TACAGCTCCACAGTACTCTGAGGCTCAAGGCGCAACCTGACAGAGTGTGTGCTGAGT 394
OY 244 GTCTGGGGGTCAAGCTGACACGACTGAATGTATGGGCGCTTCACTGCTCATTCAG 303
Db 395 GTCTGGGGGTCAAGCTGACACGACTGAATGTATGGGCGCTTCACTGCTCATTCAG 454
OY 304 AACATAGCTTCCCTCCCTTCACTCTCAAGAGCTGGCGCTTCAAGCCAGCGTGGCTGG 363
Db 455 AACATAGCTTCCCTCCCTTCACTCTCAAGAGCTGGCGCTTCAAGCCAGCGTGGCTGG 514
OY 364 GTGCTGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
Db 515 GTGCTGGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
OY 424 TGGCTGTCAAGCTGCTGCTGTGTGACAGAGCGCTATGGGGAGGTGAGATTAAGCAG 483
Db 575 TGGCTGTCAAGCTGCTGCTGTGTGACAGAGCGCTATGGGGAGGTGAGATTAAGCAG 634
OY 484 GGAACCTCTAGAGCCCTACAGCTCTCTACAGAGATGCGCCGAGAGACCGCAAGTTCG 543
Db 635 GGAACCTCTAGAGCCCTACAGCTCTCTACAGAGATGCGCCGAGAGACCGCAAGTTCG 694
OY 544 AACTTCATCTTAAGCGGAGCTGAGCGGCGCTGCGGGGTACAA--GCTCTCTCTGAGC 601
Db 695 AACTTCATCTTAAGCGGAGCTGAGCGGCGCTGCGGGGTACAAAGCTTCTCTTGAGAG 754
OY 602 ACCGCGACTCTGCGCGCGCTGAGCCCTCGCGGACCTCTTGTGTAACCTGA 655
Db 755 ACCGCGACTCTGCGCGCGCTGAGCCCTCGCGGACCTCTTGTGTAACCTGA 808
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DEFINITION mRNA sequence.
ACCESSION B1518182
VERSION B1518182.1 GI:15342974
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 791)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1455 row: 1 column: 21
High quality sequence start: 40
High quality sequence stop: 733.
Location/Qualifiers
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FEATURES
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/clone="IMAGE:5182556"
/clone_lib="NIH_MGC_116"
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BASE COUNT 134 a 257 c 265 g 135 t
ORIGIN

Query Match 49.2%; Score 606.6; DB 10; Length 791;
Best Local Similarity 98.0%; Pred. No. 2e-98;
Matches 646; Conservative 0; Mismatches 9; Indels 4; Gaps 3;

QY 579 GGGGTACAAAGCTCTTCCGTGAGACCGGACCTCTCCCGGGGTGAGCCCTC-CGCCG 637
DB 790 GGGGTACAAAGCTCTTCCGTGAGACCGGACCTCTCCCGGGGTGAGCCCTC-CGCCG 731
QY 638 ACCCTTGGTGAACCTGAGCCCTGCGCAGCCCTCATCGTGGCTTTCGAGACCTTCC 697
DB 730 ACCCTTGGTGAACCTGAGCCCTGCGCAGCCCTCATCGTGGCTTTCGAGACCTTCC 671
QY 698 TGAGCCGGGCGCTGTGTCAGCCACAGCTTCCGGGAGGGCGCTGTGCGGCTCTGAGACTCA 757
DB 670 TGAGCCGGGCGCTGTGTCAGCCACAGCTTCCGGGAGGGCGCTGTGCGGCTCTGAGACTCA 611
QY 758 CCCGAGACCCATCTTCACTTCAGAGGGCCAGAGGGC-GACCCCGGCGACCCGGCG 816
DB 610 CCCGAGACCCATCTTCACTTCAGAGGGCCAGAGGGCCTGACCCCGGCGACCCGGCG 551
QY 817 CTCGGCCT--GCTGGCCAGACCGCCACCTGGTGAACCTTGTGCTGTGAGGCCGCGCT 874
DB 550 CTCGGCCTTGTGCGCCAGACCGCCACCTGGTGAACCTTGTGCTGTGAGGCCGCGCT 491
QY 875 CCGTACCTCTTCTCGCATTTTGGAAAGTGAAGTGAAGTGGCGCTCCCGGAAGTGC 934
DB 490 CCGTACCTCTTCTCGCATTTTGGAAAGTGAAGTGAAGTGGCGCTCCCGGAAGTGC 431
QY 935 GGTACAGCCCGGTGGAAGAGACCCAGAGAGCTGTCAGAGAGAGCAAGAGACCCATGC 994
DB 430 GGTACAGCCCGGTGGAAGAGACCCAGAGAGCTGTCAGAGAGAGCAAGAGACCCATGC 371
QY 995 TGATTTCTTGAAGCGAGTCCCTGAGGGCGGGCGCTGAGACTGAGAGTGAAGCCGGAAC 1054
DB 370 TGATTTCTTGAAGCGAGTCCCTGAGGGCGGGCGCTGAGACTGAGAGTGAAGCCGGAAC 311
QY 1055 CTGAGGGGAGCTGGGTCTCGGGGGCTGTTTTGAGAGCCATCAGCTCCACCCGACA 1114
DB 310 CTGAGGGGAGCTGGGTCTCGGGGGCTGTTTTGAGAGCCATCAGCTCCACCCGACA 251
QY 1115 CCAGTGGGTCTGCTGGGAGAGACCGGAGACAGAGTGAAGTTCGATCTCGATGCT 1174
DB 250 CCAGTGGGTCTGCTGGGAGAGACCGGAGACAGAGTGAAGTTCGATCTCGATGCT 191
QY 1175 CCGGAAGTACAGTCCCGCAGAGACTTCTACTGCTGTGTCCAAAGATGATATGTAG 1233
DB 191 CCGGAAGTACAGTCCCGCAGAGACTTCTACTGCTGTGTGTCCAAAGATGATATGTAG 132

Db 190 CCGGAAGTACAGTCCCGCAGAGACTTCTACTGCTGTGTGTCCAAAGATGATATGTAG 132
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LOCUS BE792803
DEFINITION 845 bp mRNA linear EST 20-SEP-2000
601584677F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939162 5',
mRNA sequence.
ACCESSION BE792803
VERSION BE792803.1 GI:10214001
KEYWORDS EST
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 845)
NIH-MGC http://mgc.ncl.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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High quality sequence stop: 790.
Location/Qualifiers

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/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 143 a 273 c 256 g 173 t
ORIGIN

Query Match 47.8%; Score 589.8; DB 10; Length 845;
Best Local Similarity 97.8%; Pred. No. 1.9e-95;
Matches 609; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

QY 1 ATGCAAGTGTCTGATATGAGGCGCCCTGACTCTCTCCCTGGAAGACAGTCTCTG 60
DB 166 ATGCAAGTGTCTGATATGAGGCGCCCTGACTCTCTCCCTGGAAGACAGTCTCTG 225
QY 61 AGGCTTCCTTGGGAGCTCAGTGGCTGAGACTCAGAGGCTTGGGTGTCTGGGCC 120
DB 226 AGGCTTCCTTGGGAGCTCAGTGGCTGAGACTCAGAGGCTTGGGTGTCTGGGCC 265
QY 121 CACTGCTTCCTGCTTCAGTCCAGTGGCTGAAGAAGGGCTTCATTGGGAATTGGGGC 180
DB 286 CACTGCTTCCTGCTTCAGTCCAGTGGCTGAAGAAGGGCTTCATTGGGAATTGGGGC 345
QY 181 CACTACAGCTTCAGAGTACTCTGGTCAAGGCCAACCTGTCTAGAGTGTGTGTCC 240
DB 346 CACTACAGCTTCAGAGTACTCTGGTCAAGGCCAACCTGTCTAGAGTGTGTGTCC 405
QY 241 AGTGTCTGGGGGTCAACGTGACAGCACTGAAGTCTATGGGGCTTCACTGCTCCATC 300
DB 406 AGTGTCTGGGGGTCAACGTGACAGCACTGAAGTCTATGGGGCTTCACTGCTCCATC 465

Fri Nov 8 09:52:58 2002

us-09-598-443-1.rst

Page 8

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High quality sequence stop: 622.
Location/Qualifiers
1. 1067

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BASE COUNT      234 a      357 c      343 g      133 t
ORIGIN          This is a NIH_MGC Library. Note:
                ----- cracking code 019.

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Best Local Similarity	96.48;	Pred. No. 8.7e-88.		
Database Size				

	Index	Gap
QY 603	CCGGACCTCTTCGCGGCGGCTGAGCGCCCTCGGCGGACCGCTTTGGTAACCTGAGCGGC-T	661
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QY 662	GCCGAGCGCTTCATCTGATGATGCTCTTGGAGAGCGCTTCCTGAGCGGCGCTGTGACGCACA	721
Db 64	GCCGAGCGCTTCATCTGATGATGCTCTTGGAGAGCGCTTCCTGAGCGGCGCTGTGACGCACA	123
QY 722	GCTTCCGGGAGGCGCTGTCCGCGGCTGTGAGAGCTCACCGCGAGAACCATCTTATCACTCT	781
Db 124	GCTTCCGGGAGGCGCTGTCCGCGGCTGTGAGAGCTCACCGCGAGAACCATCTTATCACTCT	183
QY 782	TCGAGGCGCAGAGCGCGGACCGCCGCGACCGCGGCGCTCCGCTGTGCGCGACCGCC	841
Db 184	TCGAGGCGCAGAGCGCGGCGACCGCCGCGACCGCGGCGCTCCGCTGTGCGCGACCGCC	243
QY 842	ACCTGTGACCTTGTGCTGTGAGAGCGCGCGGCTCCGAGTACCTCTCTCCGATTTTGG	901
Db 244	ACCTGTGACCTTGTGCTGTGAGAGCGCGCGGCTCCGAGTACCTCTCTCCGATTTTGG	303
QY 902	AAGAAATGACGATGAC-G-GCTGCGCGGAAAGTGCAGTAAAGCGCGGTGGAAGAGACCC	960
Db 304	AAGAAATGACGATGACG-GCTGCGCGGAAAGTGCAGTAAAGCGCGGTGGAAGAGACCC	363
QY 961	CAGACGCAAGCTGCGAGGAGCGAACGAGACCCCATGTCATTTCTTCCGAGCGCGGATCCCTG	1020
Db 364	CAGACGCAAGCTGCGAGGAGCGAACGAGACCCCATGTCATTTCTTCCGAGCGCGGATCCCTG	423
QY 1021	GCGCGGCGCTGAGCTAGAGTGAGACCGCGACCGCTGAGGCGGAGACCTGATGTCCGAGG	1080
Db 424	GCGCGGCGCTGAGCTAGAGTGAGACCGCGACCGCTGAGGCGGAGACCTGATGTCCGAGG	483
QY 1081	CCGTGTTTTGAGAGCCATCAGTCCACCGCGACACAA-TGGGGTCTGCTGTGGGAGAGAG	1139
Db 484	CCGTGTTTTGAGAGCCATCAGTCCACCGCGACACAA-TGGGGTCTGCTGTGGGAGAGAG	543
QY 1140	CCGAGG--CAGCGAATGAGACCTTCGAGTCTCGGCTGGGAAACATCAAGTCCGCCACA	1197
Db 544	CCGAGGCGACGAAATGAGACCTTCGAGTCTCGGCTGGGAAACATCAAGTCCGCCACA	603
QY 1198	GACTTCTACTGCTGTGTCACGAAGATATATGTAG-1233	
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RESULT 11
B1759065
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FEATURES	DEFINITION
ACCESSION	603042860F1 NIH_MGC_116 Homo sapiens cDNA IMAGE:5183271 5', mRNA sequence.
VERSION	B1759065.1
KEYWORDS	B1759065.1 GI:15750643 EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
AUTHORS	1 (bases 1 to 983)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Inocyte Genomics, Inc. Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://imgc.llnl.gov Plate: L14M1451.1.gov High quality sequence: row: 6 column: 16 Location/dupe: stop: 885.

BASE COUNT	ORIGIN	023. Note: this is a NIH-MGC library.	Accession code
157 a	326 c	299 g	201 t

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Best Local Similarity	91.0%;	Pred. No. 9.3e-87;		
Matches 711; Conservative	0;	Mismatches 25;	Indels 45;	

[illegible]

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OY		419	TCAAATGCC-GTCTAACGTCGTGCTGTGGTACCAAGAGCGCATATGGAGGTGAAGATA	477
Db		637	TCAAATGCCGTGTACACTGTGCTGTGGTACCAAGAGCGCATATGGAGGTGAAGATA	477
OY		478	AACGAGCGGAAACTCTACGACGCCCTAAGTCTCTACAGCACTGCCCGAGAGCGGCAAG	537
Db		697	AAC-----GCGACTGCCCGGAGACCGCAAG	722
OY		538	TTCGTGAACCTTAATCTTAAGACCGCGAGCTGG--AGCGGCGCTCGGGGCT-ACAAGCTCTTCC	595
Db		723	TTCGTGAACCTTAATCTTAAGACCGCGAGCTGGAGCGGCGCTCGGGGCTTAACAAGCTCTTCC	782
OY		596	-TGGAGCACCGGAGCTCC-TGCGCGGCGAC-TGAGCCCCGCGCGAGCTTAAGTTGAGTACC	652
Dl		783	TTCGAGACAGCCGAGACTCTTTCGCCGCGCTTAGAGCCCTCCGCCGACTTTTGGGTGAACC	842
OY		653	TGAGCGCTGCGGAGCGCTCATCGTGTGCTTTTGGAGCGCTTCTCTGAGCCGCGGCTGGT	712
Db		843	TGAACCGGTG-CGAGCGCTCATCGTGTGCTTCCGAGCGCTTCTCTGAGCCGCGGCTTGT	901
OY		713	GCAAGCACAGCTCTCCGGAGGCGCTGTGCCGCGCTGCTGGAGCTCAACCGCGAGACCATCT	772
Db		902	GCAGACACAGGTTCCGG-AAGGCTTTTGCCCGTGTGTGAGCTCAACCGAGAACGCGATT	959
OY		773 T	773	
Db		960 T	960	
RESULT	12			
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DEFINITION	602633540F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778744 5'			
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VERSION	BG742077.1	GI:14052730		
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ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/			
UNPUBLISHED	(1999)			
Contact:	Robert Strausberg, Ph.D.			
Email:	cga@phs.fda.nhl.gov			
Tissue Procurement:	James Cleaver, M.D.			
CNA Library Preparation:	Life Technologies, Inc.			
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNLN) DNA			
Sequencing by:	Incyte Genomics, Inc.			
Clone distribution:	MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNLN at:	http://image.llnl.gov			
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High quality sequence stop:	769.			
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.				
Average insert size 1.5kb. Library constructed by Life				
Technologies. Note: this is a NCI_CGAP Library."				
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Best Local Similarity	97.1%	Pred. No. 7.6e-86		
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QY 121	CACGTCTCCCTCCCTTTCAGTCCA-GGGCTGTAAAGACGGGGCTTCCATTGGGAATGGGG 179			
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QY 240	CAGTGTCTGGGGGTCAACGTGACCA-GCAGTAAGTCTATGGGGCTTTCACCTGTCTC- 297			
Db 411	CAGTGTCTGGGGGTCAACGTGACCATGACCTAAGATCTATGGGGCTTTCACCTGTCTCG 470			
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Db 471	ATCCAGAACATAGCTCTCTCTCTTCACTCTTTCAGAGAGCTGGCCCTTCAAGCCACGT- 529			
QY 358	GCTGGGCTGCTGGCCCTCTCTGCTGCTGCTGGGCCCTCTGCTGGCCCTGTCTCTAT 417			
Db 530	GCTGGGCTGCTGGCCCTCTCTGCTGCTGCTGGGCCCTCTGCTGGCCCTGTCTCTAT 589			
QY 418	GTCAGATGCGCTCTCAACGTGCTCTGTGT-ACACAGACGGCTATGGGAGGTGAGAT 476			
Db 590	GTCAGATGCGCTCTCAACGTGCTCTGTGTGTAAACGAGACGGCTATGGGAGGTGAGAT 649			
QY 477	AAACGACGGGAAGCTCTACGACGCTACGCTCTACACAGCACTGCCCGAGGACCG-CA 535			
Db 650	AAACGACGGGAAGCTCTACGACGCTACGCTCTACACAGCACTGCCCGAGGACCGCA 709			
QY 536	AGTTCGTGAATCTTCACTTAAAGCCGACACTGGAGCGGCTGGGGCTTCAAGACTCTTCC 595			
Db 710	AGTTCGTGAATCTTCACTTAAAGCCGACACTGGAGCGGCTGGGGCTTCAAGACTCTTCC 769			
QY 596	TGGACGACCGGACCTCTGCGCGCG 622			
Db 770	TGGACGACCGGACCTCTGCGCGCG 796			
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DEFINITION	603053464P1 NIH_MGC_122	Homo sapiens	CDNA clone	IMAGE:5203070 5',
ACCESSION	Bi770099			
VERSION	Bi770099.1	GI:15761677		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 801)			
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: rsraus@nci.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 Location/Qualifiers

FEATURES

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 spleen, and 20-22 week male spleens. Library is 1190-
 primed, and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."
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 Matches 545; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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 OY 61 AGGCTGCTTGGGACCTAGTGGCTTGAAGTGCAGGCTTGGGTAGTCTCTGGGCC 120
 Db 314 AGGCTGCTTGGGACCTAGTGGCTTGAAGTGCAGGCTTGGGTAGTCTCTGGGCC 373
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 Db 374 CACTGCTCCCTGCTTACAGTCAAGTGGCTGAAGACGGGCTTCCATTGGGAATTGGGGC 433
 OY 181 CACTACAGCTTCACAGATCTCTGGTCAAGGCCAACCTTGCAGAGGTGCTGTGCC 240
 Db 434 CACTACAGCTTCACAGATCTCTGGTCAAGGCCAACCTTGCAGAGGTGCTGTGCC 493
 OY 241 AGTGTCTGGGGGTCAAGTGAACGACGACTGAAGTCTATGGGGCTTACCTGCTCATC 300
 Db 494 AGTGTCTGGGGGTCAAGTGAACGACGACTGAAGTCTATGGGGCTTACCTGCTCATC 553
 OY 301 CAGAACATCAGCTTCCCTCTTCACTCTCAGAGAGTGGCCCTTCAAGCCACAGTGGCT 360
 Db 554 CAGAACATCAGCTTCCCTCTTCACTCTCAGAGAGTGGCCCTTCAAGCCACAGTGGCT 613
 OY 361 GCGGTGCTGGGCTCCCTCTGCTGTCC -TGCCTGGCCCTGCTGTGGCGCCCTGCTATGT 419
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 OY 420 CAAGTGCCGTCAACGCTGTCTGTGTACAGAGCCGTA -TGGGAGGTGAGATTA 478
 Db 674 CAAGTGCCGTCAACGCTGTCTGTGTACAGAGCCGTA -TGGGAGGTGAGATTA 733
 OY 479 ACGAGGGAGAGCTTACAGAGCCCTAGCTCTCCTACAGAGAGTGGCCCGGAGAGCCGCACT 538
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ACCESSION mRNA sequence.
 BIR20133
 VERSION BIR20133.1 GI:15931683
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ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 783)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

AUTHORS

CONTACT: Robert Strausberg, Ph.D.
 Email: cgaubs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

COMMENT

High quality sequence stop: 701.
 Location/Qualifiers

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FEATURES

source

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 Db 404 CAGTGTCTGGGGGTCAACGCTGTGTGTACAGAGCCGTA -TGGGAGGTGAGATTA 522
 OY 300 CAGAACATCAGCTTCCCTCTTCACTCTCAGAGAGTGGCCCGGAGAGCCGCACT 538
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QY      478 AACGAGCGGAGACCTCT -ACGAGCGCTACCTCTCTACAGAGCGAGCGCGAGACCGCAA 536
Db      643 AACGAGCGGAGACCTCTACAGAGCGCTACCTATCTACAGAGCGAGCGCGAGACCGCAA 702
QY      537 GTTCTGAACCTTCACTATCTTAA -AGCCGACGCTGAGCGG -CGTGGGGGCTTACAAGCTCTTC 594
Db      703 GTACGTGAACCTTCACTATCTTAAAGAGCGGACGCTGAGCGAGCGAGCTGCGGCTTACAAGCTCTTC 762
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VERSION    B1758455.1 GI:15750033
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SOURCE      human.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE   1 (bases 1 to 821)
            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: c9apbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6
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                primed and directionally cloned (EcoRV site is destroyed
                upon cloning). Average insert size 1.5 kb, insert size
                range 1-3 kb. Library is normalized and enriched for
                full-length clones and was constructed by C. Gruber
                (Invitrogen). Research Genetics tracking code 019. Note:
                this is a NIH MGC Library."
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Best Local Similarity 99.6%; Pred. NO. 7.7e-79;
Matches 508; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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DB 731 AAGTGCGCTCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 790
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